

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 28, 2005, 08:29:34 ; Search time 660.916 Seconds
(without alignments)
15733.537 Million cell updates/sec

Title: US-09-551-494-5
Perfect score: 6355
Sequence: 1 gatgttttaataagtttttgcga.....taaccgcgtagcgccca 6355

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2468	38.8	6395	3	US-09-259-741-1
2	2468	38.8	6395	3	US-09-037-751-1
3	2468	38.8	6395	3	US-09-466-422-1
4	2468	38.8	6395	4	US-09-962-527-1
5	2466.4	38.8	6395	2	US-08-687-559-2
6	2466.4	38.8	6395	4	US-09-401-415-2
7	2455.4	38.6	6439	3	US-09-259-741-2
8	2455.4	38.6	6439	3	US-09-037-751-2
9	2455.4	38.6	6439	4	US-09-466-422-2
10	2455.4	38.6	6439	4	US-09-962-527-2
11	2452.2	38.6	6475	3	US-09-259-741-4
12	2452.2	38.6	6475	3	US-09-037-751-4
13	2452.2	38.6	6475	3	US-09-466-422-4
14	2452.2	38.6	6475	4	US-09-962-527-4
15	2449.8	38.5	6446	3	US-09-259-741-5
16	2449.8	38.5	6446	3	US-09-037-751-5
17	2449.8	38.5	6446	4	US-09-466-422-5
18	2449.8	38.5	6446	4	US-09-962-527-5
19	2431.2	38.3	6425	3	US-09-259-741-3
20	2431.2	38.3	6425	3	US-09-037-751-3
21	2431.2	38.3	6425	4	US-09-466-422-3
22	2431.2	38.3	6425	4	US-09-962-527-3
23	2286.6	36.0	7685	3	US-09-502-710-22
24	2286.6	36.0	7685	3	US-09-502-710-25
25	2286.6	36.0	7685	3	US-09-502-711-22
26	2286.6	36.0	7685	3	US-09-502-711-25
27	2286.6	36.0	7685	4	US-09-565-616A-1

28	2286.6	36.0	7686	3	US-09-502-710-23	Sequence 23, Appl
29	2286.6	36.0	7686	3	US-09-502-711-23	Sequence 23, Appl
30	2286.6	36.0	7687	3	US-09-502-710-24	Sequence 24, Appl
31	2286.6	36.0	7687	3	US-09-502-711-24	Sequence 24, Appl
32	2286.6	36.0	7688	3	US-09-502-710-27	Sequence 27, Appl
33	2286.6	36.0	7688	3	US-09-502-711-27	Sequence 27, Appl
34	2285	36.0	7926	3	US-09-500-554-1	Sequence 1, Appl
35	2285	36.0	7926	3	US-09-726-648-1	Sequence 1, Appl
36	2285	36.0	7926	4	US-10-119-330-1	Sequence 1, Appl
37	2283.4	35.9	7686	3	US-09-502-710-26	Sequence 26, Appl
38	2283.4	35.9	7686	3	US-09-502-711-26	Sequence 26, Appl
39	2283.4	35.9	7686	4	US-09-565-616A-2	Sequence 2, Appl
40	693.2	10.9	1425	1	US-08-488-672-4	Sequence 4, Appl
41	690	10.9	1425	4	US-08-708-354-4	Sequence 4, Appl
42	302.4	4.8	2173	2	US-08-553-619B-6	Sequence 6, Appl
43	270.2	4.3	1825	1	US-08-176-414B-1	Sequence 1, Appl
44	270.2	4.3	1825	2	US-08-336-724-1	Sequence 1, Appl
45	267.8	4.2	807	4	US-09-565-616A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-259-741-1
; Sequence 1, Application US/09259741
; Patent No. 6033895
; GENERAL INFORMATION:
; APPLICANT: GARGER, STEPHEN
; APPLICANT: HOLTZ, R. BARRY
; APPLICANT: MCCULLOCH, MICHAEL
; APPLICANT: TURPEN, THOMAS
; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
; PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES FROM PLANT
; TITLE OF INVENTION: SOURCES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/259,741
; FILING DATE: February 25, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/037,751
; FILING DATE: March 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 00801.0140.US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-463-8100
; TELEFAX: 650-463-8400
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6395 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic RNA
US-09-259-741-1

Query Match 38.8%; Score 2468; DB 3; Length 6395;

Db 4338 AGAAAGACCCCUCAAGGAUUUAUACCGCAGGUUAAAAACUUGCAUCUGGUUACAAGA 4397
 Qy 4382 AAAAGCGGTGATGACTTCTTCAATCGGCAATCTGTATTAATAGCAGCTTGTCTGGGT 4441
 Db 4398 AAGACGGGACGUCACGACGUUUAUUGGAACACUUGAUCUUGUGCAUGUUGGCC 4457
 Qy 4442 TCAATGTTACCGATGGAAGGTGATATAAAGGTGCTTTTGTGGAGACGATTCGGTTTTG 4501
 Db 4458 UCGAUGUCUUCGAGGAGAAUUAUUAUUAAGGAGCCUUUUGCGGACGAUUGUCUG 4517
 Qy 4502 TATTTTCCAAAGGTTGGATTTCCCTGCACATTCAGTCATGTCATCTCATGTGCAAT 4561
 Db 4518 UACUUCCAAAGGUGUGUUGUUCGGAUGUGCAACUCCCGGAUUCUUAUGUGAAU 4577
 Qy 4562 TTTGAGGCCAACTGATAGAAAGAGGTACCGTTTCTTTGTGTGTAGATACATACAC 4621
 Db 4578 UUGAGCAAAACUGUUUUAUUAUUAUUAUUGGAUUAUUGCGGAAGAUUAUUAU 4637
 Qy 4622 CATGATAGGAGCAATAGTGTATATATGATCTTTTGAAGTTGATCTCCAACTTTGGGCA 4681
 Db 4638 CACGACGAGGAUGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4697
 Qy 4682 AAACATATCAGGATATGATCACTTAGAGAGTTAAGGTGCTTTTGTGGATGTTGCT 4741
 Db 4698 AAACACAUCAAGGAUUGGGAACACUUGGAGAGUUCAGAGGUCUUCUUGUGAUGUUG 4757
 Qy 4742 TGTTCGCTCGGAACTGTGTAGGCTTTCCGACGCTGAACGACGATCTCAAGGAGGTT 4801
 Db 4758 GUUUGUU--GAACAUAUUGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4814
 Qy 4802 CATAAAACCGGATGATGTTGCTTTTAAATGTTGTTTAAACAAATTTTGTGTGAT 4861
 Db 4815 CAUAAAGCGCCCUCCAGGUCUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4874
 Qy 4862 AAATTTTATTAGACTTTTAAATGGCTGTAGTCTCAGAGATCTGTCAAAT 4921
 Db 4875 AAAGUUCUUUUAAGAGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4934
 Qy 4922 TAGCGAGTTCTTCTTCAACAGGATGAGATCTTCCGGCATTCATGACTAAGGT 4981
 Db 4935 CAUAGAUUAUACCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4994
 Qy 4982 CAAGAGTGTAGAAATACGACTGTGGAAGAGTATGCTGTGTTAAGATGATGCTTTTC 5041
 Db 4995 AAAGAGUUAUUGUUGUUCCAAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5054
 Qy 5042 TGATGTAGATTCTTAAAGTGTGTTAGTTAGTTAAGAAAGGTTATGTTGCTTAGCTGA 5101
 Db 5055 AGAGGUGAAACCUUUAAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5114
 Qy 5102 TTTGCTAGTGTCTGGGAGTGGAACTCTCCGGATAACTCCGCTGGTGTGCTAGCTTTG 5161
 Db 5115 UUGUGUCGACGCGGAGUGACUUGCCUGACAUUUGACAGAGAGGUGAGCGUGUG 5174
 Qy 5162 TATTGTAGATAAGAGATGAAGAGGTAAGGAAGCAACGCTGGGTGGTATCACGCC 5221
 Db 5175 UCUGGUGACAAAAGGAAGGAGAGCGACGAGGCCACUCUCGGAUUAUUAUUAUUA 5234
 Qy 5222 TGCTTGCAAAAGAAATTTTCTTTTAACTTAATCCCTTAATTTTCAATTAATCCGAGGA 5281
 Db 5235 AGCUGCAAGAAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5294
 Qy 5282 TGCTGAGAAGCACCGCTGGCAAGTGTAGTGAATATCAAAAGAGTGGCTATGGAAGAG 5341
 Db 5295 CGCGAUGAAACGUCUGGCAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5354
 Qy 5342 ATACTGCTCTTATCTTTTGGAGTTCGTTTCAATTTGTTGTAGTACATAAAAATATGTAAG 5401
 Db 5355 UUCUGUCGCGUUCUUGGAGUUGUUGCGUGUGUUAUUAUUAUUAUUAUUAUUAU 5414
 Qy 5402 AAAAGGTTTGAAGGAACTATTTTGTAGTGTACAGCGCTCGCAATTTGAATCACTGA 5461

Db 5415 AUUAGGUUUGAGAGAGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5474
 Qy 5462 AAAAGTGTGTGAGAGTTCGTGATGAAGTACCAATGGTGTGAACTCGAAAAGTTC- 5520
 Db 5475 AGAAGUGUUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUG 5534
 Qy 5521 -----CGAAAAAACHAAAAAAGAAATGTTAGTGAATTAATGTTAAAT- 5561
 Db 5535 AUCUGAAACCGGAAAAAGAGUAGUCCGCAAGGAAAAUUAUUAUUAUUAUUAU 5594
 Qy 5562 -----AGAAAAATAAATAACAGTGTGAAGAGGTTTTTAAATTTGAGGAAATGAGGA 5614
 Db 5595 AGUCCGCAACAGAACUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5654
 Qy 5615 TAATGTAAGTGTAGTACGAGT-----CTATCGGCTCATCGAGTACGTTTTTAATCAAT 5665
 Db 5655 UAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5711
 Qy 5666 ATGCTTTATCAATCAACTCTCGAGCAATTTGTTTACTTATCTTCCGCTTACGCAGAT 5725
 Db 5712 AUGUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5771
 Qy 5726 CTTGTGAGTGTATCAATCTGTGTACAAATGCAATTTGGGTAAACAGTTTCAAAACGCAACA 5785
 Db 5772 CCAUAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5831
 Qy 5786 GCTAGGACCAACAGTCCAAACAGCAATTTGGGTGCTCGTGGAAACCTGTGCTAGTATGACA 5845
 Db 5832 GCUCGAACTUGUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5891
 Qy 5846 GTGAGATTTCTGCTGATTCCTGATTTCTATGTATAGATATAATTTGAGCTTTCGTTG 5905
 Db 5892 GUUAGGUUCCUGACAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5951
 Qy 5906 ATCAACGCGGTTTAAATAGCTTTGATCTAGATACTAGATAATAATAGAGTTGATTAATCAA 5965
 Db 5952 GUACAGACACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 6011
 Qy 5966 CCCGCAACCGAATACTACTGAAATCGTTAACGCACTCAGAGGTAGACGATGCTACTGTA 6025
 Db 6012 GCGAAACCCACGACUGCCGAGAGCUUAUUAUUAUUAUUAUUAUUAUUAUUAU 6071
 Qy 6026 GCTATAAGGCTTCAATCAATTAATTTGGCTTAATGAATGCTGTTGTAATCGCATCTTC 6085
 Db 6072 GCCAUAAGGACCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 6131
 Qy 6086 AATCAACGAGCTTTGAGACTGTAGTGTGCTGTGACCAACAACTCCGGCTTACTTAG 6145
 Db 6132 AUUGGAGCUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 6188
 Qy 6146 CTATTGTTGTGAGATTTCTTAAATAAAGTCCGTGGAAGACTTAAATTTCAAGGTGGCTGA 6205
 Db 6189 -UGAGGUAGUACAAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 6246
 Qy 6206 TACCBAATCAGCAGTGTGTTGCTGCTCACTTAATATAATACGATTTGTCATATCTCGATCC 6265
 Db 6247 UACGAUAAACGAUAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 6305
 Qy 6266 AACAGTTTAAACCACTGTGATGCTGTATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 6325
 Db 6306 GCGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 6355
 Qy 6326 AATCCTCCCTAACCGCGCTAGCGGCCA 6355
 Db 6366 AAUCCCCCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 6395

RESULT 2
 US-09-037-751-1
 ; Sequence 1, Application US/09037751
 ; Patent No. 6037456
 ; GENERAL INFORMATION:
 ; APPLICANT: GARGER, STEPHEN

798 UUGACGAAUCAAACCGGUGUUUUUUGCGGGAUGGAGACAAGUUGACCUUUUUUUUGCA 857 Db
860 GATGAAGTACTTTAAATATATAGTCATATAATACAAATAATCTCTGCAATATGTAGTTAAA 919 Qy
858 UCAGAGAGUACUCUUAUUUUUGCAUAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 917 Db
920 TCTTACTTTCCTGCTCTAGTAGAATAGTTTACTTTTAAAGAAATTTTATAGTCACTAGGTT 979 Qy
918 ACUUAUCCCGGCUUAUAGAGAGGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 977 Db
980 AATACTTGGTTTGTAAATTTACCAAGTAGTACCTATATCTGTACAGAGTGTAGA 1039 Qy
978 AAUACCGUGUUUUGAUGUUUUUUAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1037 Db
1040 CAAGTAGGCTGTAGTAGTATGATCAGTTCTATGAGGCGATGGAAGCGCTTTGCTTTACAG 1099 Qy
1038 CAUAAAAGUUAUAGUAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1097 Db
1100 AAAACCTTTGGCCATGTTTCAACACTGAAGAGCAATCTTTTAGAGACAACGGCTTCGGTTAAC 1159 Qy
1098 AAGACUUGCAUUGGCAACAGCGAGAGAAUCCUUGAGGAUUAUUAUUAUUAUUAUUAUUA 1157 Db
1160 TTTTGGTTCCTAAGATGAAGACATGTTGATAGTACCGCTGTTTGGAGGTTCTATTACC 1219 Qy
1158 UACUGGUUCCCAAAUUGAGGGAUUGGUAUUGCAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1217 Db
1220 AGCAAAAGATGACAGAGGAGTGAGTCAATGTTTATCTGCTTCTGTTTACACAGTGT 1279 Qy
1218 ACUUAAGAGAGACCGCAAGAGAGUUAUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1277 Db
1280 AATCATATCAGAACATATCAAGCCAAAGGTTAACTTACCAAGAGCTATTATCTTCGTG 1339 Qy
1278 AACCACAUUGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1337 Db
1340 GAGTCTATAAGATCCCGGTGATATCAATGTTGTTACTGCTAGTGTCAATGGATGTA 1399 Qy
1338 GAUUGAUUUGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1397 Db
1400 GATAAGCAATCTTCAACCTTGTCAATGCTTCTTCTGACACTTAAGTCTGCTGCG 1459 Qy
1398 GACAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1457 Db
1460 CTTCAAGACGATATAGTAAATGGAAGTTTCGGTCTGTTGGTAAAGACCACTTCTGAAT 1519 Qy
1458 CUAAAGGAUGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1517 Db
1520 ATTTGGGATAGGTGGGCAAAATTTTGGAAAGCTTTTCCCACTATCAAGAGAGATG 1579 Qy
1518 GUGGGGAUGAUUUUGCGGUUGGGAACGCAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1577 Db
1580 GTGACGAGGAATTTCTGGATGTAAGTGAATGCTCTGAAGATCAAGATCCAGATCTG 1639 Qy
1578 UUGAACAGGAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1637 Db
1640 TATGTACATGGAAGAGAGGTTCTGTAGTGAATACCAAGTCTGAGAGTTTACCGCAT 1699 Qy
1638 UAUGUACCUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1697 Db
1700 CTAGATATCAAGAGGACTTAGAAGAGCTGAGCAATGTAGCAGCGGTTTATCAGAAAT 1759 Qy
1698 CUUGAUUAGGAAGAGGGAAGAACCGGAAGUGAUAUUAUUAUUAUUAUUAUUAUUAUUA 1757 Db
1760 TCTATCCTTAAGGGTCTGATTAATTTGATATCGGAATTTCAAGAGATGTGCAAGCT 1819 Qy
1758 UCGGUGUUAAGGAGGUCUGACAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1817 Db
1820 TTAGATGTTAGTCTGTGACGACGAGTAATCTGTTGAGTGGCGGAGAGATAGAAGC 1879 Qy
1818 UUGGAAGUUAACCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1877 Db
1880 GGTTTAACTCTTACTTTTATAGCCAAACCGAGGAGAAATGTGGCTTAAGGCTCT-----T 1933 Qy
1878 GGUUGACUCUCACAUUUUUAACGACCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1937 Db

1934 AAAAGCAGCGGCTCTGAGCGCGTGTGTATGTTTGAACCGACATCCGAGAGAGGTGAACGTA 1993 Qy
1938 CAAGAGAGGCUUCAGAAAGGUGCAUUGGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1997 Db
1994 AATAAATTTTCTATTGCTGAGAAAGGAGATTGCTGTGTGTGAGAAAGTCACTGTTTG 2053 Qy
1998 AUGAAGGUGCAUGGCGAGAGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2057 Db
2054 ACGAATGTAATTTAGAGCACGAGAGTTGAGTCCCTCAACGATTTTCCATAAGGCTTGC 2113 Qy
2058 GAGUGUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2117 Db
2114 GTGATAGTGTGATTAACAAGCAATGCGATCGGTTGTCTACATCTGCTCTACTCAAAGTT 2173 Qy
2118 GCAGAUUCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2177 Db
2174 CAAACAATGAGAACTATGTGCAGCAGTTTGGCAGCTTCTGTCGCGCACCTGTATCAAT 2233 Qy
2178 CAGAAAUGAAAAACUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2237 Db
2234 CTATGCAAGTCACTAAAGGATGAAGTCCGGTATGATTCTGATTCAGGAGAGAAAGTTGCT 2293 Qy
2238 CUGGUCAGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2297 Db
2294 GTTTGGGATGCTACTTTTGAAGAGTGGCTCTCTCAAACTCGCGGCAAAAGGTCATTCATGG 2353 Qy
2298 GUCUUGAUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2357 Db
2354 GGAGTTGCTGATTAACAAGGGAATGTTTACTGCACTTCTATCTTTTGAAGGAT 2413 Qy
2358 GGUGUGUUAAGAACCCACGCGAGGAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2417 Db
2414 AGAATGTTGATGAGAGCGACTGAGAGAGGCTGTATCATCTGTATCAATGCTATAT 2473 Qy
2418 GGUGUGGAGCAUGGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2477 Db
2474 TCTGATATGCAAAAGCTCAAAATCTGAGGAAAAACAATGAGAGAGCGGTGAACCCACGAA 2533 Qy
2478 UCCGACAUUGCGAAACUCAGAAACUGCGCAGACUGUUAUUAUUAUUAUUAUUAUUA 2537 Db
2534 CTTACTGAAAGATGTTACTTGTGATGGGTGCTGCTGTGTTGGAAGATTAACAAGGAT 2593 Qy
2538 AGUAGCGCAAAAGGUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2597 Db
2594 TTTGAAAGATTTGATGAGATTTGATCTGTTTCTGTTCTGGAAGAAACAAGCTGCTGT 2653 Qy
2598 CUUCCAGGGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2657 Db
2654 ATGATCAAGAAAGGCTTAATTTCTGCTGATTAAGAGCCACAATGGAACAATGTGAGA 2713 Qy
2658 AUGAUCAGAGACGUGCGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2717 Db
2714 ACGGTAGATTCATCTTCTAATGCTAT-----CCAAAACCGCATCACAGAGGCTT 2764 Qy
2718 ACCGUGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2777 Db
2765 TTTATGATGAGGTTGATGCTGACACCGGTTGTTTAACTTCTGCTGCTTATCTCT 2824 Qy
2778 UUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2837 Db
2825 GGTTCGACATCGCATATATTTACGAGATACACAGAGATTTCTTTTCAATTAACAGATT 2884 Qy
2838 UUGGCGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2897 Db
2885 CAGAAATTTCCGCTATCCAAAACATTTTGAAGCTGCAAGTGGATGAAGTTGAGATGAGG 2944 Qy
2898 UCAGAUUCCCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2957 Db
2945 AGGACCACTGAGATGCCAGGTGATGATTTTCTTCTCAATTCGAAGTACGAAGA 3004 Qy
2958 AGAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3017 Db

[illegible]

Qy	6266	AA	CAGTTTAACCATGTGATGGTGTATCTGTGTATGCGCTAAACAATCCGAGAGGTTCCG	6325
Db	6306	GC	GGGCGCAAAUAUAUAGGUUUAUAUAUCCGCGGAGCAGCUAAUAAAGCAGGGGGUUCG	6365
Qy	6326	AA	TCTCTCCCTTAACCGCCGGTAGCGGCCCA	6355
Db	6366	AA	UCCCCCGGUAACCCCGCGUAGGGGCCCA	6395

RESULT 4

US-09-962-527-1
: Sequence 1, Application US/09962527
: Patent No. 6740740
: GENERAL INFORMATION:
: APPLICANT: GARGER, STEPHEN
: HOLTZ, R. BARRY
: MCCULLOCH, MICHAEL
: TURPEN, THOMAS
: TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
: PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
: FROM PLANT SOURCES
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Howrey & Simon
: STREET: 1299 Pennsylvania Avenue N.W.
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/962,527
: FILING DATE: 24-Sep-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/037,751
: FILING DATE: 10-march-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Halluin, Albert P
: REGISTRATION NUMBER: 25,277
: REFERENCE/DOCKET NUMBER: 00801.0140.999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-463-8109
: TELEFAX: 650-463-8400
: TELEX: <Unknown>
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6395 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: unknown
: MOLECULE TYPE: Genomic RNA
: SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-962-527-1

Query Match	38.8%	Score 2468	DB 4	Length 6395
Best Local Similarity	44.6%	Pred. No. 0		

Db	1698	CTTGACATTAGGAAGAAGATGGAAGAAACGGAAGTGGATGATCAATGCACTTTCAGAGTTA	1757
Qy	1760	TCTATCCTTAAAGGGTGTGATAAATTTTCGATATCGCGAAGTTTCAAGAGCATGTGCAAGGCT	1819
Db	1758	TCGGTGTAAAGGAGTCTGACAAATTCGATGTTGATGTTTTCCTCCAGATGTGCCAATCT	1817
Qy	1820	TTAGATGTTAGTCTCTGATGTGGCAGCAGAGTAATTCGTTGAGTGGCGGAGAAATAGAAAGC	1879
Db	1818	TTGGAAGTTGACCAATGACGCGCAGCGAAGGTTTATAGTCGCGGTTCATGAGCAATGAGAGC	1877
Qy	1880	GGTTTAACTCTTACTTTTGAATGAAGCCACGAGGAGAAATGGCTAAAGGCTCT-----T	1933
Db	1878	GGTCTGACTCTCAATTTTGAACGACCTACTGAGCGAATGTGGCTAGCTTTTACAGGAT	1937
Qy	1934	AAAAAGCAGCGGTCTGAGCGCGTGTATGTCTTGAACCGCATCCGGAAGAGGTGAACGTA	1993
Db	1938	CAAGAGAAGGCTTCAGAAAGTGCTTTTGGTAGTTACCTCAAGAGAAGTTGAAGAACCGTCC	1997
Qy	1994	AATAAATTTTCTATGTGAGAAAGGAGATTTGCCTGTGTGTGAGAGAAAGTCATGGTTTG	2053
Db	1998	ATGAAGGTTTCGATGGCCAGAGGAGAGTTACAATTAGCTGTCTTGTCTGGAGATCATCCG	2057
Qy	2054	ACGAATGCTAACTTAGAGCACGAGGTTGGAGTCCCTCAACGATTTCCATAAGGCTTGC	2113
Db	2058	GAGTCGTCCTATTCTTAAGAACGAGGAGATAGAGTCTTTTAGAGCAGTTTCATATGGCAACG	2117
Qy	2114	GTGGATAGTGTGATTTACAAAGCAAAATGGCATTCGGTGTGTCTACACTGGCTCACTCAAAAGTT	2173
Db	2118	GCAGATTTCGTTAAATTCGTAAACGAGATGAGTCGATTTGTGTACACGGGTCCGANTTAAGTT	2177
Qy	2174	CAACAAATGAAGAACTATGTGGAACAGTTTGGACGTTTGTTCGCGCACTGTATCAAAAT	2233
Db	2178	CAGCAAAATGAAGAACTTTATCGATAGCTGTGAGTACACTATCTGTCTGCGGTGTGCAAT	2237
Qy	2234	CTATGCAAGTCACTAAAGGATGAGTCGGGTATGATTTCTGATTTCCAGGGAGAAAGTTGGT	2293
Db	2238	CTCGTCAAGATCCCTCAAGAGTACAGCTGCTATGACCTTTGAACCCCGTCAAAAGTTTGA	2297
Qy	2294	GTTTGGGATGTCACTTTTGAAGATGGCTCCCTCAAACTCGCGGCAAGGTTCATTCATGG	2353
Db	2298	GTCTTGGATGTTCATCTAGGAAGTGGTTAATCAACCAACGGCCAGAGTCATGCAATGG	2357
Qy	2354	GGAGTGTCTGGATTTACAAAGGGAAATGTTTACTGCACTTCTATCTTATGAAGAGAGAT	2413
Db	2358	GGTGTGTGGAACCCACGCGAGGAAGTATCATGTGGCGCTTTTTCGAAATATGATGAGCAG	2417
Qy	2414	AGAATGGTGAAGAGAGTGGAGGAGGAGTGGCTGTATCATCTGTATACAATGGTATAT	2473
Db	2418	GGTGTGGTGACATCGCGATGATTTGGAAGAAGATGAGTGTCTGAGCTCTGAGTCTGTGTTTAT	2477
Qy	2474	TCTGATATTGCAAAAGCTCCAAATCTGAGGAAACAAATGAGAGACGGTGAACCCCAAGAA	2533
Db	2478	TCCGACATGGCGAACTCAGAACTCTGCGCAGACTGTCTTGAACGGGAGAACCGCATGTC	2537
Qy	2534	CCTACTGCAAGATGGTACTTGTGGATGGGTGCTGTGGTTGTGGAAGATGACAAAGGAGAT	2593
Db	2538	AGTAGCGCAAGGTTGTCTTGTGGAACGAGTTCGGGCTCTGGGCAAAACCAAGAGAAAT	2597
Qy	2594	TTTGAAGATTTGATCTGATGAGGATTTGATCTTGGTTCTGTGGAACAGAGCTGTCTGCT	2653
Db	2598	CTTTCCAGGGTTAATTTTGTATGAAGATCTAATTTTAGTACTCTGGGAAGCAAGCCGCGAA	2657
Qy	2654	ATGATCAGAAGAGGGCTTAAATCTGGAATGATGAAGAGCACAATGGAACAATGTGAGA	2713
Db	2658	ATGATCAGAAGAGTGGCAATTCCTCAGGGATTAATTTGGGCCACGAGGACAAAGTTTAA	2717
Qy	2714	ACGGTAGATTCACTTCTTAATGCAT-----CCAAACCGCGGATCACAAAGAGGCTT	2764
Db	2718	ACCGTTGATTCTTTTCATGATGAATTTTGGGAAAAAGCACACGCTGTCAAGAGGGTTA	2777
Qy	2765	TTTATGATGAAGGGTTGATGCTGCACACCGGTTGTGTTAACTTCTCTGGTCTTATCTCT	2824

Db	2778	TTCAATTGATCAAGGGTGTGATGTTGCATACTGGTGTGTTTAATTTTCTTGTGGCGATGTCA	2837
Qy	2825	GGTTGCGACATTCGCATACATTTTACGGAGATACACAGCAGATTCCTTTCTTAAACAGAGTT	2884
Db	2838	TTGTGCGAAATTCGATATGTTTACGGAGACACACAGCAGATTCATACATCAATAGAGTT	2897
Qy	2885	CAGAAATTTCCGGTATCCCAAAACATTTTGAAGAGCTGCAAGTGGATGAAGTGGATGAGG	2944
Db	2898	TCAGGATTTCCCGTACCCCGCCCATTTTGGCAAAATTTGGAAGTTGACGAGGTGGACACGC	2957
Qy	2945	AGGACCACTAGATAGTCCCGAGGTGATGCAATTTTCTCAAAATCGAAGTACGAAGGA	3004
Db	2958	AGAACTACTCTCGTGTGTCAGCGGATGTCAACATTTCTGAACAGAGATATGAGGCG	3017
Qy	3005	GCGGTGAACCACTTCCAACTGTACACGATCGGTCTCATCTGAGATGATAGGCGGTAAAG	3064
Db	3018	TTTGTCTATGAGCACTTCTTCGGTTAAAAAGTCTGTTTCGCGAGGAGATGGTCGCGGAGCC	3077
Qy	3065	GGAGTACTAAACAGTGTTCCAAAACCACTAAAGGGGAAATTTGTAACCTTTCACTCAGGCT	3124
Db	3078	GCCGTGATCAATCCGATCTCANAAACCTTCATGGCAAGATCCCTGACTTTTACCCCAATCG	3137
Qy	3125	GATAAAATTTGAGTTAGAGGAGAGGGCTATAAGAAATGTGAACACCGTTTCATGAGATCCAA	3184
Db	3138	GATAAGAAAGCTCTGCTTTCAAGAGGTATTCAGATGTTTACACTGTGCATGAAGTGCAA	3197
Qy	3185	GGAGAAACCTTTGAAGATGTGCTGGTTCAGATTTGACGGCAACTCCCACTGACTCTGAT	3244
Db	3198	GGCGAGACATCTCTGATGTTTCACTAGTTAGGTTAACCCCTACACCAGTCTCCCATATT	3257
Qy	3245	TCCAGTCTTCCCGCATGTTCTAGTCGCTCTGACTAGACACACAAAGAGGCTTCAAAATAT	3304
Db	3258	GCAGGAGACGCCACATGTTTGGTCGCAATGTCAAGGCACACCTGCTCGCTCAAGTAC	3317
Qy	3305	TACACCTGATGTTAGATCCTTTAGTACAGATAATAGTGAATTTGTTCTTTTAAAGCTCC	3364
Db	3318	TACACTGTTGTATGATCTTTTGTAGTTAGTATCATTAGAGATCTAGAGAACTTTAGTCTG	3377
Qy	3365	TTCTTTTGAAGATGATATGTTAGAGAGGAGTGTAGTAGTGAATTTACAGATGATGATGCA	3424
Db	3378	TACTTGTAGATATGATAAGGTGCGATGAGGAGCAACAATAGCAATTTACAGATTTGACTCG	3437
Qy	3425	GTGTTCAAGGTATATATCTTTTGTGGCAACCTTAATTCAGGAGACTTTTCCAGATCTA	3484
Db	3438	GTGTTCAAGGTTTCCAACTTTTGTGTCAGCGCCAAAGACTGGTGATATTTCTGATATG	3497
Qy	3485	CAGTTCTTATTCAGATGATGCTCCCTGGTAAATAGTACTATATCTTAAACAAGTATGATGCT	3544
Db	3498	CAGTTTACTATGATAAGTGTCTCCAGGCAACAGCACCATGATGATTAATTTTGTATGCT	3557
Qy	3545	GTTACCATGAGGTTACGTGATAATAGTCTTAAATGTGAAGGATTTGTGTTCTTGTATTTTCC	3604
Db	3558	GTTACCATGAGGTTGACTGACATTTTCAATGATGTCAAAGATTCATATTTGGATATGTCT	3617
Qy	3605	AAAAGTATTCGATGCCAAGAGGAGTCAAACTGTCTAGAGCCAGTTTTCGCTACCGCG	3664
Db	3618	AAAGTCTGTCGCGCTAAGGATCAAAATCAAACTTAATACCTATGATGGTACGAAACGCG	3677
Qy	3665	GCGAACCAGGAGGCTGAGGACTACTCGAAATCTGGTTGCAATGATTAATAAGAAAT	3724
Db	3678	GCAGAAATGCAACGCCAGACTGGACTATTTGGAAATTTTAGTGGCATGATTAATAAGGAC	3737
Qy	3725	TTCAACGCCACAGACCTGACGGGGAACGATGACATTTGAGAGCACCGCATCTGTTGTAGTA	3784
Db	3738	TTTAAACGACCCGAGTGTCTGGCATCATTTGATATTTGAAATACTGCACTCTTATAGTTGA	3797
Qy	3785	GATAAGTTTTTGTAGTACTATTTTATAAAGAGAAATATACAAAATAATTTTGTCTGGA	3844
Db	3798	GATAAGTTTTTGTAGTATTTTGTCTTAAAGAAAGAAACCAAAATAAATAATTTTCT	3857
Qy	3845	GTGATGACGAAGGATTCATATGATGAGATGGTTGGAAACAGGAAAGATCTATTTGGAC	3904
Db	3858	TTGTTAGTAGAGAGTCTCTCAATAGATGTTTAGAAAAAGCAGGAACAGGTAACAATAGGC	3917

QY 3905 GACTTGGCTAACTACAAATTTTACAGATCTGCGGCCATCGATCAGTACAGACACATGATC 3964
 Db 3918 CAGCTCGCAGATTTTGAATTTTGTAGATTTGCCAGCAGTTGATCAGTACAGACACATGAT 3977
 QY 3965 AAGGCTCAACCAAAACAGAAATTTGACCTTTTCAATTCAGAAATGAATACCTGCTCTGCA 4024
 Db 3978 AAGACACAAACCAAGCAAAATTTGACACTTCAATCCAAACGAGTACCCGCTTTGCA 4037
 QY 4025 ACAATGCTACCAATTCGAGCAGATCAACGCTATTTTGGCCGTTTCTCA---GAGCTT 4081
 Db 4038 ACGATTTGTGTACATTTCAAAAAGATCAATGCAATATTTGGCCGTTTGTAGTACGCTT 4097
 QY 4082 ACAAGTTGCTGCTCGAGCAATTTGATTTCTAAGAGTTTCTTTTCTTTACTAGGAAACT 4141
 Db 4098 ACTAGGCAATTAAGCAGTGTGATTCGACAGATTTTGTGTTTTCACAAAGAGACA 4157
 QY 4142 CCAGAACAGATTCAGAAATTTTCTCGGATCTCGACTCGCAGTTCCTATGATGTGTTA 4201
 Db 4158 CCAGCGCAGATTTGAGGATTTCTTCGGAGATCTCGACAGTCAATGCGGATGATGCTTTG 4217
 QY 4202 GAACCTGATTTCTTAAGTATGATAGTCAACAGACGAGTTTCAATTTGCTGCTGATGAT 4261
 Db 4218 GAGCTGGATATATCAAAATACGACAAATCTCAGATGAATTCACGTGCGAGTAGAATAC 4277
 QY 4262 GAAATATGAAAAGATTGGGTCTCAATGAGTTTGGCCGAGTGTGGAAACAAAGGCGAC 4321
 Db 4278 GAGATCTGGGAGATTTGGTTTGAAGCTTCTTGGGAGAGTTTGGAAACAAAGGCGAT 4337
 QY 4322 AGGAAACAACTTTGAAGGATTAATTTGCTGGAATCAAGACATGCTGTGGTATCAAGG 4381
 Db 4338 AGAAGACCACTTCAAGGATTAATCCGCGAGTATAAAACTTGCATCTGGTATCAAGA 4397
 QY 4382 AAAAGCGGTGATGATCTACTTCTATCGGCAATACCTGTTATTAATAGCAGCTTGGT 4441
 Db 4398 AAGAGCGGGACGTCACGAGTTTCAATTTGGAACACTGTGATCAATCTGCTCATTTGGCC 4457
 QY 4442 TCAATGTTACCGATGAAAGGTCATAAAAGGTCTTTTGTGGAGACCATTCGGTTTGG 4501
 Db 4458 TCGATCTCTCGATGAGAAATTAATCAAGAGGCTTTTGGGTGAGCAGATGCTGCTG 4517
 QY 4502 TATTTTCCAAAGGTTTGGATTTCCCTGACATTCAGTCAATGCTATCTCATGTGGAAT 4561
 Db 4518 TACTTTCCAAAGGTTTGGATTTCCGATGTGCAACACTCCGCGAATCTTATGTGGAAT 4577
 QY 4562 TTTGAGCGCAACTGTATAGAAAGAGTACGTTACTTTTGTGGTATGATACATCATACAC 4621
 Db 4578 TTTGAAGCAAACTGTTTAAAAAACAGTATGGATACCTTTTGGGAGAGATATGTAATACAT 4637
 QY 4622 CATGATAAGGAGCAATAGTATATGATCTTTCGAAGTTGATCTCCAAACTTTGGGCA 4681
 Db 4638 CAGCAGAGGATGCAATTTGATATAGATCCCTTAAAGTTGATCTCGAACTTTGGTGT 4697
 QY 4682 AAACATATCAAGGATTTATGATCACTTTAGAAGAGTTAAGGGTGTCTTTTGTGCGATGTGCT 4741
 Db 4698 AAACATCAAGGATTTGGGAACACTTTGGAGAGTTTCAAGAGGTTCTCTTTGTGATGTGCT 4757
 QY 4742 TGTTCGCTCGAAACTGTGCTTAGGCTTTCCGACGCTGAACCGACGTATCAAGGAGTT 4801
 Db 4758 GTTTCGTT---GAAACAATTTGCGGTATTAACACAGTTTGGACGACGCTGTATGGGAGTT 4814
 QY 4802 CATAAACCGGATGATGTTGCTGCTTTTAAATTTGTTAAACAAATTTTGTGCTGAT 4861
 Db 4815 CATAGACCGCCCTCCAGGTTCTGTTTGTATTAAGAGTCTGTTGAGTATTTTGTCTGAT 4874
 QY 4862 AAATTTTATTTAGAACTTTGTTTAAATGGCTGTGTAGTCTCAGAGATCTCTCAAAAT 4921
 Db 4875 AAAGTTCTTTTGAAGTTTGTATAGAGTCTTAGTGTGTTAAGGAAAGAGTATAT 4934
 QY 4922 TAGCGAGTTTCATTTGATCTTTTGAACAGGATGATACCTTTCCGGCATTTCAATGATG 4981
 Db 4935 CAATGAGTTTATCGACTGACAAAAATGGAGAGATCTACCCGTCGATGTTTACCCCTGT 4994

QY 4982 CAAGAGTGTTAGAATATTCGACTGTGGACAGATTAATGGCTGTTAGAATGATAGTCTTTC 5041
 Db 4995 AAAGAGTGTATGTGTCTCCAAAGTTGATAAAATATATGGTTTATGAGAAATGAGTCAATGTC 5054
 QY 5042 TGATGTAGATTTTACCTTAAAGGTGTTAAGTTAGTTAAGAAAGGATGTGTGTCTTACGCTGA 5101
 Db 5055 AGAGGTGAACCTTCTTAAAGGAGTTTAACTTATTTGATAGTGTAGTGTGTGTGTACCGG 5114
 QY 5102 TTTGTGTAGTGTCTGGGAGTGGAAATCTCCCGGATTAATCTCCGCTGTGTGTGTGTGTGTGT 5161
 Db 5115 TTTGT 5174
 QY 5162 TATTGTAGATGAAGAAATGAAGAGTGAAGAGCAACGCTGGGTGTGTGTGTGTGTGTGTGTGT 5221
 Db 5175 TCTGTGTGACAAAGGATGGAAGAGCCGACGAGGCCACTCTCTCGGATCTTTACTACACAGC 5234
 QY 5222 TGCTTGGCAAAAGAAATTTTCTTTTAAAGCTATCTCTTAACTTAACTTAACTTAACTTAACT 5281
 Db 5235 AGCTGCAAGAAAGATTTTCAAGTTCAGGTCTTCAATTTTCAATTTTCAATTTTCAATTTTCA 5294
 QY 5282 TGCTGAGAGCAACCGCTGTGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5341
 Db 5295 CGCGATGAAGAAAGCTCTGCAAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5354
 QY 5342 ATACTGTCTTTTATCTTTGGAGTTCGTTTCAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 5401
 Db 5355 TTTCTGTCTGCTTTCTCTGGAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5414
 QY 5402 AAAAGTTTGGGGAACGTTATTTTTCAGTGTGACAGCGCTCGCCAAATTTGAACTCACTCA 5461
 Db 5415 ATTAGTTTGGAGAGAAAGTTTACAAACGTGAGAGACGAGGCGCCATGGAATCTTACAGA 5474
 QY 5462 AAAAGTTTGTGAGGAGTTCGTGATGAAAGTACCAATTTGCTGTGTGTGTGTGTGTGTGTGT 5520
 Db 5475 AGAAGT 5534
 QY 5521 -----CGGAAAAACAAAAAGAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5561
 Db 5535 ATCTCGAACCGGAAAAAGAGTGTCTCGCAAGGGAAAAATAGTAGTAATGATCGGTC 5594
 QY 5562 -----AAGAAAAATAATACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5614
 Db 5595 AGTCCGCAACAGAACTATAGAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5654
 QY 5615 TAATGTAGT 5665
 Db 5655 TAATTTTATCGATGATGT 5711
 QY 5666 ATGCTCTTATACAACTCACTCTCCGAGCCAAATTTGTGTGTGTGTGTGTGTGTGTGTGTGT 5725
 Db 5712 ATGTCTTACAGTATCACTACTCCATCTCAGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5771
 QY 5726 CTTGTGCTGATCAATCTGT 5785
 Db 5772 CCAATAGAGTTAATTAATTTATGTACTAATGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 5831
 QY 5786 GCTTAGGACAAAGTCTCAACAGCAATTTGCGGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 5845
 Db 5832 GCTCGAAGT 5891
 QY 5846 GTGAGATTTCTGCTGATCGGATTTCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5905
 Db 5892 GTTAGGTTCCCTGACAGT 5951
 QY 5906 ATCAAGGCTTATTAATAGTCTTGT 5965
 Db 5952 GTACAGCACTGT 6011
 QY 5966 CCGCAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 6025
 Db 6012 GCGAACCCGACGCTGCGGAAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6071
 QY 6026 GCTATAAGGCTTCAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 6085

[illegible]

RESULT 6

```

US-09-401-415-2
; Sequence 2, Application US/09401415
; Patent No. 6503732
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS TO
; PRODUCE PEPTIDES AND PROTEINS
;
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,415
; FILING DATE: 21-Sep-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01467
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bostich, June M.
; REGISTRATION NUMBER: 31,238
; REFERENCE/DOCKET NUMBER: FD-4074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6395 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: TWV
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..6395
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-401-415-2

```


QY 1040 CAAAGTAGGTGTGATAGTACAGTCTATAGGCGATGGAAGACGCGCTTCTTCTTACAG 1099
 Db 1038 CATAAAGTGTAGATAGTACAGTCTTATCTGCAATGGAAGACGCGATGCGATACAAA 1097
 QY 1100 AAAACCTTGGCCATGTTCAACTGAAGAGCAATCTTTAGAGACACGGCTTCGGTTAAC 1159
 Db 1098 AAGACTCTTGCATGTGCAACGAGGAGAAATCCTCTTTGAGGATTCATCATCACTCAAT 1157
 QY 1160 TTTTGGTTCCTTAAGATGAAGACATAGTGTAGTACCGCTGTTTGAGGGTCTTATATACC 1219
 Db 1158 TACTGGTTCCTCAAAATGAGGATAGTGTATCTGATACCAATATTCGACATTTCTTTGGAG 1217
 QY 1220 AGCAAAAAGATGACAAAGGAGTCAAGTCAATGTTAAATCGTGACTTCGTTTACAGTGCTT 1279
 Db 1218 ACTAGTAGAGGACGCGCAAGGAGTCTTAGTGTCCAAGGATTTCTGTTTACAGTGCTT 1277
 QY 1280 AATCATATCAGAAATATCAACCCAAAGGTTAACTTACCAGAAAGTATATCTTTCTGTTG 1339
 Db 1278 AACCACATTCGAACATACACAGGCAAGGCTTTACATACGCAAAATGTTTGTCTTCTTGTTC 1337
 QY 1340 GAGTCTATAAGATCCCGGTGATATCAATGATGTTTACTGTAGGTCTGAATGGGATGTA 1399
 Db 1338 GAATCGATTCGATCGAGGGTAATCAATAACGGTGTGACAGCGAGGTCGAAATGGGATGTG 1397
 QY 1400 GATAAGCAATTTCTCAACCTTGTCAATGACTTTCTTCTTGCAGACTAAGCTGGCTGG 1459
 Db 1398 GACAAATCTTTGTACAAATCTTTGTCATGACGTTTACCTGCATATAAGCTTGCCTGTT 1457
 QY 1460 CTTCAAGACGATATAGTAATGGAAAGTTTCGGTGTCTGGATAGACACATCTTCTGAATTT 1519
 Db 1458 CTTAAAGGATGACTTACTGATTAAGCAAGTTTAGTCTCGGTTTCGAAACCGGTGCGCAGCAT 1517
 QY 1520 ATTTGGGATGAGTGGGCAAAATTTTGTGAAAGCTTTTCCCACTATCAAGAGAGATGTG 1579
 Db 1518 GTGTGGATGAGATTTCCGTGCGGTTTGGGAAGCAATTTCCCTCGTGAAGAGAGGCTC 1577
 QY 1580 GTGACGAGGAAATTTCTGGATGTAAGTGAAGATGCTCTGAAGATCAAGATCCAGATCTG 1639
 Db 1578 TTGAACAGGAAATTTATCAGATGTCGAGCGAGCGCATTAGAGATCAGGGTGCCTGATCTA 1637
 QY 1640 TATGTCAATGGAAGACAGGTTGCTGATGTAATACCAAGTCTGAGGAGTTACCGCAT 1699
 Db 1638 TATGTGACCTTCCACACAGATTTAGTGAATGAGTACAGGCGCTCTGTGACATGCTCGG 1697
 QY 1700 CTAGATATCAAGAGGACTTAGAAGAGCTGAGCAAAATGTCAGCGCTTATCAGAAATTA 1759
 Db 1698 CTTGACATTAAGGAAGATGGAAGAAACGGAAGTGTATCAATGCACTTTACAGATTA 1757
 QY 1760 TCTATCCTTAAGGGTCTGATTAATTTTCGATATCGGAAAGTTCAAAGACATGTGCAAGGCT 1819
 Db 1758 TCGGTGTTAAGGGAGTCTGACAAATTCGATGTTGATGTTTTCAGAGATGCGCAATCT 1817
 QY 1820 TTAGATGTTTATGCTGTGAGAGACGAGTAAATCGTTGCGATGTCGAGGAGGATAGAGC 1879
 Db 1818 TTGAAGGTTGACCAATGACGCGAGCGAAGGTTATAGTCCGGTCTATGAGCAATGAGAGC 1877
 QY 1880 GGTTTAACTTCTTACTTTTCAATGACCAACCGAGGAGATGTGCTAAAGCTCT-----T 1933
 Db 1878 GGTCTGACTCTCACATTTTGAACGACCTACTGAGGCGAAATGTTGCGGTAGCTTTTACAGGAT 1937
 QY 1934 AAAAGACGCGGTCTGAGGCGGTGTTATGTTCTTGAACCGACATCCGAGAGGTGAAACGTA 1993
 Db 1938 CAAGAGAAGGCTTCAGAGGTGCTTTGGTAGTTTACCTCAAGAGAGTTGAGAAACCGTCC 1997
 QY 1994 AATAAATTTTCTATCTGAGAAAGGAGATTCCTGTGTGTGTCGAGAAAGTCAATGGTTTG 2053
 Db 1998 ATGAAGGGTTCGATGCGCAGAGGAGAGTTACAAATTAGCTGGTCTTCTGCGAGATCATCG 2057
 QY 2054 ACGAATGCTAACTTAGACACAGGAGTTGGAGTCCCTCAACGATTTTCCATAGGCTTGC 2113
 Db 2058 GAGTCGTCTATTTCTTAAGAACGAGGAGATAGAGTCTTTTAGAGAGGTTTCTATATGGCAACG 2117
 QY 2114 GTGGATAGTGTGATTACAAAGCAAAATGGCATCGGTTGTCTACACTGGCTCACTCAAAGTT 2173

Db 2118 GCAGATTCGTTAAATTCGTAAGCAGATGAGCTCGATTTGTGTACACGGGTCGATTAAGGTT 2177
 QY 2174 CAAACAAATGAAGAACTATGTGGACAGTTTGGCAGCTTGTGTGTCCGCCACTGTATCAAAAT 2233
 Db 2178 CAGCAATGAANAACCTTTATCGATAGCCTGTGATAGCATCACTATCTGCTCGGTGTGCAAT 2237
 QY 2234 CTATCAAGTCACTAAAGGATGAAGTCGGGTATGATTTCTGATTCAGGGAGAAAGTTGGT 2293
 Db 2238 CTGTCGAAGTCTCTCAAGATACAGCTGCTATTGACCTTGAACCCGCTCAAAAGTTTGA 2297
 QY 2294 GTTTGGGATGTCACTTTGAAAGAGTGGCTCTCAAACTGCGCGCCCAAGGTCATTCATGG 2353
 Db 2298 GTCTTGGATGTGCACTAGGAAGTGGTTAAATCAAAACCAACGCGCAAGAGTCATGATGG 2357
 QY 2354 GGAGTTGCTCTGGATTACAAAGGGGAAAATGTTTACTGCACCTTCTATCTTATGAAGAGAT 2413
 Db 2358 GGTGTTGTGAAACCCACGCGAGGAGTATCATGTGGCGCTTTTGGAAATATGATGAGCAG 2417
 QY 2414 AGAATGGTGACTGAGAGCGACTGAGGAGGGTGTGATCATCTGATATCAATATGATATAT 2473
 Db 2418 GGTGTTGTGACATGCGATGATTTGGAGAAAGTAGCTGTCACTCTGAGTCTGTGTTTAT 2477
 QY 2474 TCTGATTTGCAAGCTCAAAATCTGAGGAAAACAATGAGAGACGCTGAACCCCAAG 2533
 Db 2478 TCCGACATGGCGAAACTCAGAACTCTGCGCAGACTGCTTCGAAACGAGAAACCGCATGTC 2537
 QY 2534 CCTACTGCAAGATGCTACTTGTGATGGGGTCCCTGTTGGTGGAAAAGTACAAAGAGAT 2593
 Db 2538 AGTAGCGCAAGGTTGTTCTTGTGACGAGGTTCCGGGCTGTGGGAAACCAAGAAATTT 2597
 QY 2594 TTTGAAAAGATTTGATCTTGTGAGGATTTGATCTTTGGTTCCTTGGAAAACAAGCTGCTG 2653
 Db 2598 CTTTCCAGGGTTAAATTTTGTGATGAAGATCTAAATTTAGTACCTTGGGAAACGAGCGGAA 2657
 QY 2654 ATGATCAGAAAGGCTTAATTCATCTGCACTGAAGAGCACAAATGACAAATGTGAGA 2713
 Db 2658 ATGATCAGAAAGCGTGGCAATTTCTCAGGGATTTATTTGGGCCACCAAGAGCAACGTTAAA 2717
 QY 2714 ACGGTAGATTCTACTTCTAATGCTAT-----CCAAAACCGCATCACAAAGAGGCTT 2764
 Db 2718 ACCGTTGATTTCTTTCATGATGATTTTGGGAAAAGCAACGCTGTCAAGTCAAGAGTTA 2777
 QY 2765 TTTATTTGATGAAGGGTTGATGCTGCACACCGGTGTGTAACTTCTGCTGTCTTCTCT 2824
 Db 2778 TTTCAITGATGAAGGGTTGATGTTGATGCTGTTGTTAAATTTCTTGTGCGGATGTCA 2837
 QY 2825 GGTTCGGAATCGCATACATTTTACCGAGATACACAGCAGATTCCTTTTCAATTAACAGATT 2884
 Db 2838 TTTGTCGAAAATTTGCATATGTTTACCGAGACACACAGCAGATTTCCATACATCAATAGATT 2897
 QY 2895 CAGAAATTTCCGTTATCCCAACATTTTTCGAGAGCTGCAAGTGAAGTTCAGATGAGG 2944
 Db 2898 TCAGGATTTCCGTTATCCCGCCATTTTTCGCAAAATTTGGAAGTTGACAGGTGAGACACGC 2957
 QY 2945 AGGACACACATGAGATGCGCCAGGTGATGTAATTTTCTTCAATTCGAAGTACGAAGA 3004
 Db 2958 AGAACTACTCTCGGTGTTCCAGCCGATGTCAACATTTATCTCAAAGAGATATGAGGCG 3017
 QY 3005 GGGGTGACAAACACTTTTCAACTGTACACGATCGGTCTCATCTGAGATGATAGCGGTAG 3064
 Db 3018 TTTGTGATGAGCACTTCTTTCGGTTTAAAGTCTGTTTCGAGGAGATGTTTCGCGGAGCC 3077
 QY 3065 GGAGTACTTAAACAGGTTTCCAAAACCACTTAAAGGGGAAATTTGTAATTTTCACTCAGGCT 3124
 Db 3078 GCGGTGATCAATCCGATCTCAAAACCTTTGATGCGAAGATCCTGACTTTTACCAATCG 3137
 QY 3125 GATAAATTTGAGTTAGAGGAGGAGGCTTATAAGAAATGTGAACACCGCTTCAATGAGATCCAA 3184
 Db 3138 GATAAAGAGCTCTGCTTTCAAGAGGTTATTCAGATGTTTCACTGTGATGAAGTCAAA 3197
 QY 3185 GGAGAAACCTTTTGAAGATGTTGCTGCTGATGAGCGGCAACTCCACTGACTCTGATT 3244

Db 3198 GGGGAGACATCTCTGATGTTTCACCTAGTTAGGTTAAACCCCTACACACAGTCTCCATCATTT 3257
Qy 3245 TCCAAGTCTTCCCGCATGTTCTAGTCGCTCTGACTAGACACACAAAGAGCTTCAATAT 3304
Db 3258 GCAGGACAGCCACCATGTTTGGTCGCATTTGTGCAAGGCACACCTGTTCCGCTCAAGTAC 3317
Qy 3305 TACACCGTAGTGTAGATCTCTTTAGTACAGATTAATAGTGAATTTGTCTCTTTTAAGCTCC 3364
Db 3318 TACACTGTGTTATGAGTACCTCTTAGTTAGTTATCATTTAGAGATCTAGAGAAACTTTAGCTCG 3377
Qy 3365 TTCCCTTTTAGAATGTATGTTAGAGCAGGAGTGTAGATAGCAATACAGATGAGATGCA 3424
Db 3378 TACTTGTGTAGATATGATAAGGTCGATGCGAGGAACAATAGCAATTTACAGATTTGACTCG 3437
Qy 3425 GTGTTCAAAGGTCATAATCTCTTTGTGGCAACACCTAAATCAGGAGACTTTTCCAGATCTA 3484
Db 3438 GTGTTCAAAGGTTCCATCTTTTGTGTCAGCGCCAAAGACTGGTGATATTTCTGATATG 3497
Qy 3485 CAGTTCTATTACGATGTATGCTCCCTCGGTAATAGTACTATATCTTAACAAGTATGATGCT 3544
Db 3498 CAGTTTACTATGATAAGTGTCTCCAGGCAACAGCACCATGATGAATAATTTTGTATGCT 3557
Qy 3545 GTTACCATGAGGTTACGTGATAATAGTCTTAATGTGAAGGATTCGTCTTTGATTTTTC 3604
Db 3558 GTTACCATGAGGTTGACTGACATTTCAATGTAATGTCAAGATTCGAATTTGGATATGCT 3617
Qy 3605 AAAAGTATTCGGATGCCAAAGGAGGTGAACCATGTCTAGAGCCAGTTTTCGCTACCGCG 3664
Db 3618 AAGTCTGTGTCGCTTAAAGATCAAAATCAACCACTAATACCTATGGTAGCAAGCGCG 3677
Qy 3665 GCGGAACCGCCAAAGGCGTCAGGACTACTCGAAATCTGGTTGCAATGATTAAGAANAAT 3724
Db 3678 GCAGAAATGCCACCAGACTGGACTATTGGAATAATTTAGTGGCGATGATTAAGAAGAAC 3737
Qy 3725 TTCAACCCACAGACCTCGAGGACGATTTGACATTCGAGACACCGCATCTGTTGTAGTA 3784
Db 3738 TTTAACGCCCGGAGTGTCTGGCATCATTTGATATTTGAANAATCTGCACTCTTTAGTTGTA 3797
Qy 3785 GATAAGTTTTTGTAGTACTATTTTATTAAGAAAGAAATAACACAAATAATTTGCTCGA 3844
Db 3798 GATAAGTTTTTGTAGTATTTGCTTAAAGAAAGAAACCAATAATAAATGTTTCT 3857
Qy 3845 GTGATAGCAAGGATTCATGATGAGATGTTGAAACACAGAAAGTACTATTGGAC 3904
Db 3858 TTGTTCAGTAGAGATCTCTCAATAGATGTTGAGAAAGCAGGAACAGGTAAACATAGGC 3917
Qy 3905 GACTTGGCTAACTACAATTTTACAGATCTGCGGCCATTCGATCAGTACAGACACATGATC 3964
Db 3918 CAGCTCGCAGATTTTGTATTTGTAGATTTGCCAGCAGTTGATCAGTACAGACACATGATT 3977
Qy 3965 AAGGCTCAACCAACAGAAATTCGACCTTTCAATTCAGAAATGAATACCCCTGCTCTGCAA 4024
Db 3978 AAAGCACAACCAAGCAAAATTTGACACTTCAATCCAAACGGAGTACCCGGCTTTGCGAG 4037
Qy 4025 ACAATTTGCTACCATTCGAACGACATCAACGGTATTTTGGCCGGTTTCTCA -- GAGCTT 4081
Db 4038 ACGAATTTGTACCAATTCAAAAAAGATCAATGCAATATTTGGCCCGTTGTTAGTGAGCTT 4097
Qy 4082 ACAAGGTTGCTGCTCGAGGCAATTTGATTTCTAAGAAATTTCTTTTCTTACTAGCAAACT 4141
Db 4098 ACTAGGCNAATTTACTGGACAGTGTGATTCGAGCAGATTTTGTGTTTTCACAAGAAAGACA 4157
Qy 4142 CCAGAACAGATTCAGAATTTTCTCGGATCTCGACTCGCAGCTTCTATGGAATGTTGTTA 4201
Db 4158 CCAGCGCAGATTGAGGATTTCTCGGAGATCTCGACAGTCTCATGTGCCGATGGAATGCTTG 4217
Qy 4202 GAACTGGAATTTCTAAGTATGATAAGTCAAGAACGAGTTTCAATGTGCTGTAGAGTAT 4261
Db 4218 GAGCTGGATATATCAAAATACGACAAATCTCAGAATGAATTTCCACTGTGCGAGTAGAATAC 4277
Qy 4262 GAAATATGGAAGAGTTGGGTCTCAATGAGTTTTTGGCCGGAAGTGTGGAAACAAGGGCAC 4321
Db 4278 GAGATCTGGCGAAGATTTGGGTTTTGAAGACTTCTTTGGGAGAGTTTGGAAACNAGGCGAT 4337

Qy 4322 AGGAAACAACTTTTGAAGGATTHACATTTGCTGGAATCAAGACATGTTCTGTGTTATCAAGG 4381
Db 4338 AGAAAGACCACCCCTCAAGGATTAACCGCAGGTATAAAAACTTGGCATCTGGTATCAAGA 4397
Qy 4382 AAAAGCGGTGATGCTACTCTTTTCATCGCAATACTGTTATATAATAGCAGCTGCTCTGGGT 4441
Db 4398 AAGAGCGGGACGCTACGAGGTTTCATTGGANAACACTGTGATCATTTGCTGATGTTTGCC 4457
Qy 4442 TCAATGTTTACCGATGGAAGAGGTCATAAAAGGTGCTTTTTTGTGGAGACGATTCCTGTTTG 4501
Db 4458 TCGATGCTTCCGATGGAGAAATAATCAAAAGGAGCCCTTTTGGCGTGACGATAGTCTGCTG 4517
Qy 4502 TATTTTCCAAAGGTTTGGATTTCCCTGACATTTCACTGATGCTGCTATCTCATGTGGAAT 4561
Db 4518 TACTTTCCAAAGGTTTGTGAGTTTCCGATGTCGAACACTCCGCAATCTTATGTGGAAT 4577
Qy 4562 TTTGAGGCCAAACTGTATAGAAAGAGTACGGTTACTTTTTGTGTAGATACATCATACAC 4621
Db 4578 TTTGAGCAAAACTGTTTAAAAACAGTATGGATACCTTTTGGGAAGATATGTAATACAT 4637
Qy 4622 CATGATAAGGAGCAATAGTGTATTATGATTCCTTTGAAGTTGATCTCCAAACTTGGGCA 4681
Db 4638 CACGACAGAGATGCAATGTTGTTATACGATCCCTAAAGTTGATCTCGAAACTTGGTGCT 4697
Qy 4682 AAACATATCAAGATTTATGATCACTTAGAAGATTAAGGTGCTCTTTGTGGATGTTGCT 4741
Db 4698 AAACATATCAAGATTTGGGAACACTTTGGAGAGTTTCAGAAAGGTTCTCTTTGTGATGTTGCT 4757
Qy 4742 TGTTCGCTCGAAACTGGTCTTTAGGCTTTCCGACGCTGAACGACGCTATCAAGAGGTT 4801
Db 4758 GTTTCGTT --- GAACAATTTGCGGTATTACACAGTTTGACGACGCTGTATGGGAGGTT 4814
Qy 4802 CATAAAACCCGATTTGATGTTTCGTTTCTTTTAAATTTGTTTAAACAAATTTTGTGTGAT 4861
Db 4815 CATAAGACCCGCCCTCCAGGTCGTTTGTATTATAAAAGTCTGGTGAAGTATTTGCTGAT 4874
Qy 4862 AAATTTTTTATAGACTTTGTTTAAATGGCTGTTAGTCTCAGAGATCTGTCAAAAT 4921
Db 4875 AAAGTTCTTTTGAAGTTTGTTTTATAGATGGCTCTAGTTGTTTAAAGGAAAGTGAATAT 4934
Qy 4922 TAGCGATTCATTTGATCTTTTCGAAACAGGATGAGATCTTTCCGCAATTCATGACTAAGGT 4981
Db 4935 CAATGAGTTTATCGACTGACAAATAATGGAGAGATCTTACCGTCGATGTTTACCCTGT 4994
Qy 4982 CAAGAGTGTAGAAATFCGACTGTGGAACAAGTATGCGCTGTTTAAAGAAATGATGCTTTC 5041
Db 4995 AAAGAGTGTATGTTGTTCCAAAGTTGATAAAATAATGGTTTCAAGAGAAATGATGCTTC 5054
Qy 5042 TGATGTAGATTTACTTTAAAGTGTTTAGTTAGTTTAAAGAAAGGATGCTGTGCTTAGCTGA 5101
Db 5055 AGAGGTGAACCTTCTTAAAGGATTAAGCTTATTTAGTAGGATACGCTGTTTGTAGCCGG 5114
Qy 5102 TTTGGTAGTCTGCGGAGTGGAACTCTCCGGAATACTCGCGTGGTGGTGTGCTGAGTTTG 5161
Db 5115 TTTGGTGTGTCGCGGCGAGTGGAACTTGCCTGACAAATTCAGAGGAGGTGTGACGCTGTG 5174
Qy 5162 TATTTGTAGATAAGAGAAATGAAAGGAGTAAGGAAGCAACGCTGGGTGCGTATACGCCCC 5221
Db 5175 TCTGTTGGAACAAAGGATGGAAAGAGCGGACGAGGCCACTCTCGGATCTTACTACACAGC 5234
Qy 5222 TGCTTGCAAAAGNAATTTTCTTTTAAAGCTTAATCCCTAAATTTTCAATAACATCCGAGGA 5281
Db 5235 AGCTGCAAGAAAGAAAGATTTTCAGTTCAAGGTCGTTCCCAATTAATGCTATACACCCAGGA 5294
Qy 5282 TGCTGAGAAGCACCCGTCGGCAAGTGTGTAGTGAATATCAAAAGGAGTGGCTATGGAAGAG 5341
Db 5295 CGCATGAAAAA CGTCTGGCAAGTTTGTAGTTTAAATATTAGAAAATGTAAGATGTGACGCGG 5354
Qy 5342 ATACTGTCCTTTATCTTTTGGAGTTCGTTTCAATTTTGTGTAGTACATAAAAAATATGTAAG 5401
Db 5355 TTTCTGTCGCGTTTCTCTGGAGTTTGTGTGCGTGTGATTTGTTTATAGAAATAATATAAA 5414

Qy	5402	AAAAGGTTTGAGGGAAACGTAATTTTGGTGTGACAGACGGCTCCCACTTGAACCTACTGA	5461
Db	5415	ATTAGGTTTCAGAGAGAAGATTACAAACGTGAGAGACGGAGGGCCCATGAACTTACAGA	5474
Qy	5462	AAAGGTTGTTGACGGAGTTCGTGTGATGAAGTACCAAATGGCTGTCAAACCTCGAAAGGTTTC	5520
Db	5475	AGAAGTCGTTTGATGAGTTTCATGGAAGATGTCCCTATGTGTGATCAGCGCTTGCAAAAGTTTCG	5534
Qy	5521	-----CGGAAAAACAAAAAGAAATGGTGTAGGTAAATATGTTTAATAAT	5561
Db	5535	ATCTCGAAACCGGAAAAAAGAGTGTCTCCGCAAAAGGCAAAAAATAGTAGTAATGATCGGTC	5594
Qy	5562	-----AGAAAAATAATAACAGTGGTAGAGGGTTTAAATATGAGAAATTCAGGAATTCAGGA	5614
Db	5595	AGTGCCGACACAGAAGACTATAGAAATGTTAAGGAATTTTGGAGGAATGAGTTTTTAAAAAGAA	5654
Qy	5615	TAATGTAAGTGTAGCAGAGT-----CTATCGCGCTCATCGAGTACGTTTTTAATCAAT	5665
Db	5655	TAATTTAAATCGATGATGATTCGGAGGCTACTGTGCGCAATCGAATCGTTTTT-----AAT	5711
Qy	5666	ATGCGTTATACAAATCAACTCTCCGAGCCAAATTTGTTTACATTCTTCCTCCGCTTAGCAGAT	5725
Db	5712	ATGCTTTACAGTATCACTACTCCATCTCAGTCTGCTGTCTTGTGTATCAGCGCTGGGCGCAC	5771
Qy	5726	CTGTGCGAGCTGATCAATCTGTGTACAAATGCAATGGGTAAACAGTTTCAAAACGCAACAA	5785
Db	5772	CCAATAGAGTTAAATTAATTTATGTACTAAATGCGCTTAGGAATCAGTTTTCAACACAAACAA	5831
Qy	5786	GCTAGGACAAACAGTCCAAACAGCAATTTGCGGATGCTCTGGAAACCTGTGCTAGTAGACAA	5845
Db	5832	GCTCGAACTGTCGTTCAAAGACAAATTCAGTGAGGTGTGGAAACCTTCACCAAGAATACT	5891
Qy	5846	GTGAGATTTCCTGCATCCGAATTTCTATGTGTATAGATATAATTTTCGACGCTTGATCCGTTG	5905
Db	5892	GTTAGGTTCCCTGCACAGTGACTTTAAGGTGTACAGGTACAAATCGGCTATTAGACCCGCTA	5951
Qy	5906	ATCACGGCGTTATTAAATAGCTTTTGATCTAGAAAATAGAAATATAGAGTTTGATATATCAA	5965
Db	5952	GTCAACAGCACTGTTAGTGTCAATTCGACACTAGAAATAGAAATATAGAAATTGAATTCAG	6011
Qy	5966	CCGCGACCGGAATACTACTGAAATCGTTTAAACGCACTCAGAGGGTAGACGATGCTACTGTA	6025
Db	6012	CGGAACCCACGACTGCGGAAACGTTAGATGCTACTCGTAGAGTAGACGACGCAACGGTG	6071
Qy	6026	GCTATAGGGGTTCAATCAATTAATTTGGCTAATGAACTGCTTGTGGAACTGGCATGTTTC	6085
Db	6072	GCCATAGGAGCGCGATAAATTTTAATAGTAGAATTTGATCAGAGGAACCGGATCTTAT	6131
Qy	6086	AAATCAACGAGCTTTTGAGACTGCTAGTGGAGTCTGTCTGGACCAACACTCCGGGCTACTTAG	6145
Db	6132	AATCGGAGCTCTTTCGAGAGCTCTTCTGGTTTGGTTTGGACCTCTGCTCTGCAACT---	6188
Qy	6146	CTATTGTTGTGAGATTTTCTTAAAAATAAGTCGCTGGAAGACTTAAAAATTCAGGGTGGCTGA	6205
Db	6189	-TGAGGTAGTCAAGATGCATAATAAATAACGATTTGTCCGTAAATCACA-CGTGGTGGCG	6246
Qy	6206	TACCAAAATCAGCAGTGGTTGTTTCGTCACCTTAATATACGATGTGTATATCTGGATCC	6265
Db	6247	TACGATAACGCATAGTGTTTTCCCTCCACTTAATCGAAAGGGTGTG-TGCTTGGATCGC	6305
Qy	6266	AACAGTTTAAACCATGTGATGTTATCTGTGTGTATGCGGTAAAAACATCGGAGAGGTTTCG	6325
Db	6306	GCGGGTCAATGTATATATGTTTCAATATACATCCGACGACGCACTAATAAGCGAGGGTTCG	6365
Qy	6326	AATCCTCCCTTAACCGCGGTAGCGGCCCA	6355
Db	6366	AATCCCGCGTTACCCCGGTAGGGGCCCA	6395

RESULT 7

RESULT /
US-09-259-741-2

US-09-239-741-2
; Sequence 2, Application US/09259741

; Patent No. 6033895

Db 2538 AGUAGCGCAAGGUGUUCUUGUGACGAGUUCUGCGGUGUGGAAAAACCAAGAGAAU 2597
Qy 2594 TTTGAAAGATTGATCTTGATCAGAGATTGATCTTGTTCTCGGAAAAACAAGCTGCTGT 2653
Db 2598 CUUCCAGGUGUAUUUUGAAGAGUAUCUAUUUUGUAUCCUGGGAAGCAGCCGGNA 2657
Qy 2654 ATGATCAGAAGAGGCTAATTCTCTGAGCTGATAAGAGCCACAATGGACAATGTGAGA 2713
Db 2658 AUGAUCAGAAGAGCGGGAUUCUCAGGGAUUAUUGUGGCCACGAGGACCAACGUTAAA 2717
Qy 2714 ACGGTAGATTCTCTTAATGATCCAAAACCGCGATCACA-----CAAGAGGCTT 2764
Db 2718 ACCGUGAUUCUUAUGAUGAAUUUUGGGAAGACACGCGUCAGUUAAGAAGGUUA 2777
Qy 2765 TTTATTGATGAAGGTTGATCTGCACACCGGTTGTAACTTCTGCTGCTTCTCT 2824
Db 2778 UUAUUGAAGAGGUGUGAUGUUAUCUGGUGUGUUAUUUCUGUGGCGAUGUCA 2837
Qy 2825 GGTTCGCACATCCGATACATTTACGGAGATACACAGAGATTCTTTCAATTAAACAGATT 2884
Db 2838 UUGUGGAAUUGCAUUGUUAUCGAGACACACAGCAUUAUCCAUACAUAUAGAGUU 2897
Qy 2885 CAGAAATTCCTGATATCCAAAACATTTTGAAGAGCTGCAAGTGGATGAAGTTGAGATGAGG 2944
Db 2898 UCAGGAUUCGCGUACCCCGCCCAUUAUUGCCAAUUGGAUUGACGAGGUGGAGACAGC 2957
Qy 2945 AGGACACACTGAGATGCCAGGTGATGTGAATTTTCTTCAATCGAAGTACGAAGCA 3004
Db 2958 AGAAUAUUCUGUGUGUGCGCGAUGUCACAUUAUUCUGAA CAGGAGAUAGGGC 3017
Qy 3005 GCGGTGACAAACCACTTCAACTGTATACACGATCGGTCTCATCTGAGATGATAGCGGTAAAG 3064
Db 3018 UUGUCUAGAGCAUUCUUGGUUAAAGUCUUGUCCGAGGAGAGUGGCGCGAGCC 3077
Qy 3065 GGAGTACTAAACAGTGTTCAAAACCACTAAAGGGGAAATGTGTAATCTTCACTAGGCT 3124
Db 3078 GCGUGAUAUCCGGAUCCAAAACCCUUGCAUGGCAUGAUCUGAUCUUUAUACCCAAUGC 3137
Qy 3125 GATAAATTTGAGTTAGGAGAGGCTATAGAAATGTGAACACCGTTCTATGAGATCCAA 3184
Db 3138 GAUAAAGAGAGCUGUCUUAAGAGGUAUUCAGUUGUACACUCUGUGCAUGAUGGCAA 3197
Qy 3185 GGAGAAACCTTTGAAGATGTGCTGCTGATGATGACGCGCAACTCCACTGATCTGTATT 3244
Db 3198 GCGGAGACAUACUUGAUGUUAUUAUUGGUUAUACCCCUACACAGCUUCCAUAU 3257
Qy 3245 TCCAGTCTTCCCGCATGTTCTAGTCGCTCTGACTAGACACACAAAGAGCTTCAAATAT 3304
Db 3258 GCAGGAGACAGCCCAUUGUUGUGGCAUUGUCAAAGGCACACCUUGUGGCUCAAGUAC 3317
Qy 3305 TACACCGTAGTGTAGATCTTTAGTACAGATAATTTAGTGTATTTCTTTTAAGCTCC 3364
Db 3318 UACACUGUUGUUAUGAUCUUAUUGUUAUUAUUGAUAUCUAGAGAAACUUAGCUGC 3377
Qy 3365 TTCTTTTGAATGTATGTTAGGAGAGGAGTGTAGTAGCAATTAACAGATGATGCA 3424
Db 3378 UACUUGUUAUUAUUAUAGGUGGAGUGCAGGAAACACAUAGCAUUAUACAUUGACUG 3437
Qy 3425 GTGTTCAAAGGTATATCTCTTTGTGGCAACACCTAAATCAGGAGACTTCCAGATCTA 3484
Db 3438 GUGUCAAAGGUUCCAAUUCUUUUGCAGCGCCAAAGACUGUGUAUUAUUCUGAUAUG 3497
Qy 3485 CAGTTCTATTACATGATGCTCCCTGTTAGTACTATCTTAAACAGTATGATGCT 3544
Db 3498 CAGUUUAUUAUUAUAGUGUCUCCCGAGGCAACAGCAUUAUUAUUAUUAUUAUUGU 3557
Qy 3545 GTTACCATGAGTTACTGTATATAGTCTTAATGTGAAGATTGTCTTTGATTTTTC 3604
Db 3558 GUUAUUAUUAUUAUAGUGUACAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3617
Qy 3605 AAAAGTATTCGATGCCAAAGGAGGTGAACACCATGCTTAGAGGCGAGTTTTCGTCGCG 3664
Db 3618 AAGUCUUGUGCGCCUAGGAUCAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3677

Qy 3665 GCGGAACCGCCCAAGGGCTGCGAGGACTACTCGAAAAATCTGGTTGTCAATGATTAAGAAAT 3724
Db 3678 GCGAAAAUGCCACGCGCAGACUGACUAUUGGAAAAUUAUGCGCAUGAUAUAAAAAACA 3737
Qy 3725 TTCACGACACAGACCTGACCGGGGACGATTGATTTGAGAGCACCGCATCTCTGTGTAGTA 3784
Db 3738 UUAACGCGCCGAGUGUGUGCGCAUCAUUGAAUAUUGAAAUACUGCAUUCUUGGUUA 3797
Qy 3785 GATAAGTTTTTTGATAGCTATTATTAATAAAGAAAAATAACAATAAATAATTGCTGGA 3844
Db 3798 GAUAAGUUUUUGAUGUUUAUUGCUAAAGAAAAAGAAACCAAAUAAAAUUGUUUCU 3857
Qy 3845 GTGATGACGAAGGATTCAATGATGATGGTTGGAAAAACAGAAAGAGTACTATTGGAC 3904
Db 3858 UUGUUCAGUAGAGAGUCUCUCAAUAGUGUUUAGAAAAAGCAGGAACAGGUAACAAGGC 3917
Qy 3905 GACTTGGCTAACTACAATTTTACAGATCTGCCGCATCGATCAGTACAGACACATGATC 3964
Db 3918 CAGCUCGAGAUUUUGAUUUUGUGAUUUGCAGCAGUUGAUCAGUACAGACAUAGUU 3977
Qy 3965 AAGGCTCAACAAAAACAGAAATTGGACCTTTCAATTCAAGATGAATACCTCTCTGCAA 4024
Db 3978 AAGACAAACCCAAACAAAGUUGGACACUACAUAUCCAAACGAGUAUCCCGCUUGCAG 4037
Qy 4025 ACAATTGTCTACCATTTGGAAGCAGATCAACGATATTTTGGCCGGTTCT---CAGAGCTT 4081
Db 4038 ACGUUGUGUACCAUUAUAAAAAGAUCAUAGCAUAUUCGCGCCGUGUUAUGAGUCUU 4097
Qy 4082 ACAAGTTGCTGCTCGAGCATTTGATTTCTAAGAGATTCTTTCTTTTACTAGGAAACT 4141
Db 4098 ACUAGCAUAUACUGGACAGUGAUCGAGCAUUAUUGUUUUUUAACAAGAAAGACA 4157
Qy 4142 CCAGAACAGATTCAAGAAATTTTCTCGGATCTCGACTCCGACGTTCTTCTATGATGTGTTA 4201
Db 4158 CCAGCGCAGUUGAGAUUUUUCCGAGAUUCUGACAGUUGCGGAGUGGAGUGUUG 4217
Qy 4202 GAACTGGATATTCTAAGTATGATTAAGTCAAGAACGAGATTTTCATGTCTGTGAGTAT 4261
Db 4218 GAGCUGUAUAUUAUAAAAUACGACAAAUUCAGAGAAUUAUCCAGUGCAGUAGAUAC 4277
Qy 4262 GAAATATGAAAAAGATTGGTCTCAATGATTTTGGCGAAGTGTGGAACAAGGGCAC 4321
Db 4278 GAGUUCUGCGAAGAUUGGUGUUUGAAGACUUCUUGGAGAGAAUUGUUAACAAGGGCAU 4337
Qy 4322 AGAAAAACAATTTGAAGGATTACATTGCTGGAATCAAGACATGTCTGTGTTATCAAAG 4381
Db 4338 AGAAAGACCCCUCAAGGAUUAUACCGCAGGUUAUAAAAUUAUUGCAUUGUUGGCC 4397
Qy 4382 AAAAGCGGTGATGTACTTTTCATCGGCAATACTGTTATATAGCAGCTTGTCTGGGT 4441
Db 4398 AAGGCGGGGACGUCACGACGUCAUUGGAAACACUUGAUAUUAUUGCAUUGUUGGCC 4457
Qy 4442 TCAATGTTACCGATGAAAAAGGTATAAAAGGTGCTTTTGTGGACACGATTCGTTTG 4501
Db 4458 UCGAUCUUCGCGAAGAAAAUAAUCAAAGGAGCCUUUUUGGUGAGCAUAGUCUGCUG 4517
Qy 4502 TATTTTCAAAGGTTTGGATTTCCTGACATTTCACTGATGCTTAATCTCATGTGGAAT 4561
Db 4518 UACUUUCCAAAGGUGUGAGUUUCCGGAUGUGCAACACUCCGCAUUAUUAUUGGAU 4577
Qy 4562 TTTGAGGCCAACTGTATAGAAAAGGTACGGTTACTTTTGTGGTATAGATACATACAC 4621
Db 4578 UUAAGCAAAACUGUUUAAAAACAGUAUGGAUUAUUAUUGGAAAGAUUAUUAUACU 4637
Qy 4622 CATGATAAGGGACAAATAGTGTATGATCTTTTGAAGTTGATCTCCAACTTGGGCA 4681
Db 4638 CAGACAGAGGAGCAUUGUUAUUAACGATCCUCAAAGUUGAUCUCCGAAACUUGUGCU 4697
Qy 4682 AAACATATCAGGATTATGATCACTTAGAAGAGTGAAGGTTTGTGTCGATGTGCT 4741
Db 4698 AAACAUCAAGGAUUGGAAACACUUGGAGGAGUUCAGAAAGGUCUCUUUGAUGUUGCU 4757

; TOPOLOGY: unknown
 ; MOLECULE TYPE: Genomic RNA
 US-09-037-751-2

[illegible]

Db 2058 GAGUCGUCCUAUUCUUAAGAACGAGGAGCAUAGAGUUCUUAAGAGCAGUUUUAUUAUGGCGACG 2117
Qy 2114 GTGGATAGTGTGATTACAAAGCAAAATGGCATCGGTGTCTACACTGGCTCACTCAAAGTT 2173
Db 2118 GCAGUUCGUUUAUUCGUAAGCAGAGCAGUCGUAUGUGUACACGGGCGGUAUAAGU 2177
Qy 2174 CAACAAATGAAGAACTATGTGGACAGTTTGGCAGCTTCTGTTCCGCCACCTGTATCAAT 2233
Db 2178 CAGCAAAUGAAAAUUCUUAUGCAUAGCCUGUAGCAUCAUAUCUGCGUGGUGCAU 2237
Qy 2234 CTATGCAAGTCACTAAAGGATGAAGTCGGGTATGATTCTGATTCAGGAGAGAAAGTTGGT 2293
Db 2238 CUCGUCAGAAUCCUCAAAGUAACAGUCUAUUGAUCUUGAAGAACCCGCUCAAAGUUGGA 2297
Qy 2294 GTTGGGATGTCACTTTGAAAAAGTGGCTCCTCAAACTCGCGGCAAAAGTTCATTCATGG 2353
Db 2298 GUCUGAUGUUGCAUCUAGGAGUGGUUAUCAAACCAACGCGCAAGAGUCAUGCAUG 2357
Qy 2354 GGAGTTGCTGGATTACAAGGGGAAAATGTTTACTGCACTTCTATCTTATGAAGGAT 2413
Db 2358 GGUGUUGUAGAAACCCACGCGAGGAAGUUAUCAUGUGCGCUUUGGAAUUAUGAGCAG 2417
Qy 2414 AGAATGTGTAGCTGAGAGCGACTGAGGAGGTGCTGTATCATCTGATACAATGGTATAT 2473
Db 2418 GGUGUGGUGACAUCGGAUUAUGGAGAGAGUAGUCUUAUGCUCUGAGUCUGUUGUUUAU 2477
Qy 2474 TCTGATATTGCAAAAGCTCCAAAATCTGAGGAAAAAATGAGAGACGGTGAAACCCACGAA 2533
Db 2478 UCCGACAUUGCGAAACUCAGAAACUCUGCGCAGACUGUCUUGAAACGCGAAGACCGAUGUC 2537
Qy 2534 CCTACTCAAAAGATGTTACTTGTGGATGGGTGCTGTTGTGGAAAGTACAAAGGAT 2593
Db 2538 AGUAGCGAAAGGUGUUCUUGUGACGGAAGUUCGCGGUGUGGAAAAACCAAGAAAU 2597
Qy 2594 TTTGAAAGATTGATCTTGATGAGATTGATCTTGCTGTGAAAAAAGCTGCTGCT 2653
Db 2598 CUUCCAGGGUUAUUAUGAAGAUUAUUAUUAUGUACUUGGAGAAAGCGCGGAA 2657
Qy 2654 ATGATCAGAAAGAGGGTAAATTCATCTGGAATGATAGAGCCAAATGGAATGTGAGA 2713
Db 2658 AUGAUCAGAGACGUGCGAAUUCUCAGGGAUUAUUGGCGCACGAAGGCAACGUAUA 2717
Qy 2714 ACGTGATTCATCTTAATGTCATCCAAACCGCGATCACA-----CAGAGGCTT 2764
Db 2718 ACCGUAGUUCUUAUGAUGAAUUUUGGGAAAAAGCACGCGUCAGUUCUUAAGGUUA 2777
Qy 2765 TTTATTGATGAAGGTTGATCTGCACACCGGTTGTGTTAACTTCTCGTGTCTTATCTCT 2824
Db 2778 UUCAUUAUGAAGGUGUAGUUGCAUCUUGUUGUUAUUAUUAUUAUUGGCGCAUGUCA 2837
Qy 2825 GGTTCGACATCGCATATTTACGGAGATACACAGCAGATTCCTTTTCATTAAACAGATT 2884
Db 2838 UUGUGGAAAAUUGCAUUAUUAUCGAGACACACAGCAGAUUCCAUCAUCAUAUAGAU 2897
Qy 2885 CAGAAATTCGGTATCCCAACATTTTGAAGAGTGCAGAGTGAAGTGAATGAGTAGG 2944
Db 2898 UCAGGAUUCGGAUCCCGCCCAUUAUUGCCAAUUGGAUUGACGAGGUGGAGACACGC 2957
Qy 2945 AGGACCACTGAGATGCCAGGTGATGTGAATTTTTTCTTACAAATCGAAGTACGAAGGA 3004
Db 2958 AGAACUACUCCUGUUGCAGCGCAUGUACAUUAUUAUGAAGCAGGAGUAUGAGGC 3017
Qy 3005 GCGGTGACAAACCTTCAACTGTACAACGATCGGTCTCATCTGAGATGATAGCGGTAAAG 3064
Db 3018 UUUUGAUGAGCAUCUCUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3077
Qy 3065 GGAGTACTAAACAGTGTTCAAAACCACTAAAGGAAAAATTTGTAATTTTCACTCAGGCT 3124
Db 3078 GCCGUGAUCAUCCGUAUCCUAAACCCUUGCAUGCAAGUCCUGACUUUAUCCAAUUG 3137
Qy 3125 GATAAATTTGAGTAGAGGAGAGGGCTATTAAGAAATGTGAACACCGCTTCATGAGATCAA 3184
Db 3138 GAUAAAGNAGCUGUCUUAUUAAGAGGGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3197

Qy 3185 GGAGAAACCTTTGAAGATGTGCTGGTCCAGATTGACGGCAACTCCACTGACTCTGATT 3244
Db 3198 GCGGAGACAUACUCUGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3257
Qy 3245 TCCAAGTCTTCCCGCATGTTCTAGTCGCTCTGACTAGACACACAAGAGCTTCAAAATAT 3304
Db 3258 GCAGGACAGCCCAUAUUUUUGUGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3317
Qy 3305 TACACCTAGTGTAGATCCTTTAGTACAGATAATTAAGTGAATTTGTTCTTTAAAGTCC 3364
Db 3318 UACACUGUUAUGAUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3377
Qy 3365 TTCTTTTGAAGATGTATGTTAGAGCAGGTAGTAGCAATTTACAGATGAGTGA 3424
Db 3378 UACUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3437
Qy 3425 GTGTTCAAAGTCTAATCTCTTTGTGGCAACACCTAAATCAGAGACTTTCCAGATCTA 3484
Db 3438 GUGUUAACAGGUCCAAUUAUUUUUGUGCAGCGCAAGACUGUGUAUUAUUAUUAUUAUUA 3497
Qy 3485 CAGTTCTATTACGATGTATGCTCCCTCGTGAATAGTACTATATCTTAACAAGATGATGCT 3544
Db 3498 CAGUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3557
Qy 3545 GTTACATGAGGTTACGTGATAATAGTCTTAATGTGAAGGATTTGTTCTTGTATTTTCC 3604
Db 3558 GUUACCAUGAGGUGUAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3617
Qy 3605 AAAAGTATTCGATGCAAAAGAGGAGTGAACCATGCTAGAGCCAGTTTTCGCTACCGCG 3664
Db 3618 AGUCUUGUUGCGCCUUAAGGAUCAAUCAAACCUAAUUAUUAUUAUUAUUAUUAUUAUUA 3677
Qy 3665 GCGGAACCGCAAGGGCTCGAGACTACTCGAAAATCTGTTGCAATGATTAAAGAAAT 3724
Db 3678 GCAGAAUUGCCACGCCAGACUGGACUUAUUGGAAAAUUUAUAGGCGAUGAUUAUUAAGAA 3737
Qy 3725 TTCAACGCCACAGACCTGACGGGACGATGATGATGAGAGCAGCGCATCTGTTGTAGTA 3784
Db 3738 UUAACGCCACCGAGUUGUCUGCAUCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3797
Qy 3785 GATAAGTTTTTGATAGTATTTTATTAATAAAGAAAAATACACAAAAATATTCGTGGA 3844
Db 3798 GAUAAGUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3857
Qy 3845 GTGATGACGAAGATTCAATGATGAGATGTTGGAAAAACAGGAAGAAAGTACTATTGGAC 3904
Db 3858 UUGUUCAGUAGAGAGUCUCUCAUAUAGUUGUUAAGAAAGCAGGAACAGGUAAACAUAAGGC 3917
Qy 3905 GACTTGGCTAACTACATTTTACAGATCTCGCGCCATCGATCAGTACAGACCATGATC 3964
Db 3918 CAGCUCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3977
Qy 3965 AAGGCTCAACAAAAACAGAAATTTGGACCTTTCAATTGAGAAATGAATACCTGCTCTGCAA 4024
Db 3978 AAAGCACACCCAAACAAAGUUGGACAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4037
Qy 4025 ACAATTGTCTACATTCGAAAGCAGATCAACGGTATTTTGGCCGGTTTCT---CAGAGCTT 4081
Db 4038 ACNAUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4097
Qy 4082 ACAAGGTTGCTGCTCGAGGATTTGATTTCTAAGNAGTTTCTTTCTTTTCTAGGAAACT 4141
Db 4098 ACUAGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4157
Qy 4142 CCAGAACAGATTCAGAAATTTTCTCGGATCTCGACTCGCAGCTTCCCTATGGATGTGTA 4201
Db 4158 CCAGCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4217
Qy 4202 GAATGATATTTCTAAGTATGATAGTCAAGAACGAGTTTCAAGAGTTTCTGCTGTAGATAT 4261
Db 4218 GAGCUGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4277

4262 GAAATATGAGAAAGATGGGTCTCAATGAGTGTGTCGCGAAGTGTGGAACAAGGGCAC 4321
4278 GAGAUUGGCGCAAGAUUGGUGUUUGAAGACUUCUUGGGAGAGUUGGAAACAAGGCAU 4337
4322 AGGAAACAACATTTGAAGGATTAATTGCTCGAATCAAGACATGCTGTGTGTATCAAGG 4381
4338 AGAAAGACCAACCCUACAGGAUUAUACCGCAGUAUAAAAUUCUGCAUCUGGUAUCAAGA 4397
4382 AAAAGCGGTGATGTGACTTCTCATCGCAATACTGTTATAATAGACGCTTGTCTGGGT 4441
4398 AAGAGCGGGACGUCACACGACUUCUUGGAAACACUGUGAUCUUCUGCAUGUUGGCC 4457
4442 TCAATGTTACCGATGGAAGAGGTCAATAAGAGTGTCTTTTGTGGAGACGATTCGGTTTTG 4501
4458 UCGAUGCUUCGAGGAGAAUAUAUACAAGAGCCUUCUUGCGUGACGUAUGUCUG 4517
4502 TATTTTCCAAAGGTTTGGATTTCCCTGACATTCAGTCATGTGCTAATCTCATGTGGAAT 4561
4518 UACUUCCAAAGGUGUGAGUUCGCGAUGUGCAACUCCGCGAAUUCUUAUGGAAU 4577
4562 TTTGAGGCCAACTGTATAGAAAGAGGTACGGTTACTTTTGTGTTAGATACATCATAC 4621
4578 UUUGAAGCAAAACUGUUUAAAAACAGUAUGAUAUUUUUGCGGAAGAUUGUAUAU 4637
4622 CATGATAGGCGCAATAGTGTATATGATCTTTGAAGTGTATCTTCTGAGTGTGAGTAT 4681
4638 CACGACAGAGUACUUGUUAUUAUACGACCCUUAAGUUAUUCUGGAAACUUGUGCU 4697
4682 AAACATATCAAGGATATGATCACTTAGAAGTTAAGGTTGCTTTTGTGCGATGTTGCT 4741
4698 AAACACAUCAAGGAUUGGAAACACUUGGAGAGUUCAGAAAGGUCUUCUUGUGAUGU 4757
4742 TGTTCGCTCGGAACTGTGTCTAGGCTTTCGCGAGCTGAACGACGCTATCAAGGAGTT 4801
4758 GUUUGUUGAACAAUUGUGCGUA---UUAACACAGUUGGACGCGUGUAUGGGAGUU 4814
4802 CATAAACCGGATGATGTTGCTGTTGTTTAAATGTTGTTAAACAAATTTTGTGTGAT 4861
4815 CAUAAAGCCGCCUCCAGGUGUUGUUAUAAAGUUGGUAAGUUAUUGUCUAG 4874
4862 AAATTTTATTTAGAACTTTGTTTAAATGCTGTTAGTCTCAGAGATATCTGTCAAAAT 4921
4875 AAAGUUCUUUUAAGAUUGUUAUAGUGGUCUAGUUGUUAAGGAAAGAAUGAAU 4934
4922 TAGCAGTTCATGATCTTTGAAACAGATGAGATCTTCGCGATTCATGACTAAGT 4981
4935 CAAUGAUUUUACGACCUCAAAAGAGAGAAUUCUACCGUGAUGUUUACCCUGU 4994
4982 CAAGAGTGTAGAAATATGACTGTGCAAGATTAAGGATTAAGGATGATGATCTTTC 5041
4995 AAAGAGUUGUUUUGUUCUAAAGUUAUAAUUAUUGUUAUUGGUAUGAGUACUAGUC 5054
5042 TGATGTAGATTTACTTAAAGGTTTAAAGTTAGTTAAGAAAGGATATGTTGCTTAGCTGA 5101
5055 AGAGGUGAACCUUCUUAAGGAGUUAAGUUAUAGUAGUAGUAGUACUUCUUAAGCGG 5114
5102 TTTGTAGTGTCTGGGAGTGAATCTCCGATTAATCTCCGCTGTTGTTGCTGAGTGTG 5161
5115 UUGUGUCGACCGGCGAGUGGAAUUGCCUGAACAAUUGAGAGAGGAGGUGUGUGUG 5174
5162 TATTTGTAGATAAGAAATCAAAAGGAGTAAGGAACGACGCTGGGTGCTATCAGCCGCC 5221
5175 UCUGGUGGCAAAAGGAUAGAAAGAGCCGACGAGGCAUUCUGGAUUAUUAACACAGC 5234
5222 TCGTTCGCAAAAGAAATTTTCTTTTAAGCTAATCCCTAATTAATCAATAACATCCGAGA 5281
5235 AGCUGCAAGAAAGAAUUCAGUUAAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 5294
5282 TCGTGAAGACGCCGTGCGAAGTGTGTAGTAATATCAAGAGAGTGGCTATGGAAGAGG 5341
5295 CGCGAUGAAAGAACGUCGCGAAGUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5354
5342 ATACTGTCCTTTATCTTTGAGGTTTCGTTTCAATTTGTGTAGTACATAAAAAATAATGTAAG 5401

5355 UUUCUGCCGUUCUUCUGGAGUUUGUGUGCGGUGUAUUGUUUAUAGAAAUAAUAAA 5414
5402 AAAAGTTTTCAGGGAACGTTATTTTGTAGTGTGACACAGCGCTCGCAATTTGAATCACTGA 5461
5415 AUUAGGUUUUAGAGAGAGAAUUAUCAAACGUGAGAGACGAGGGCCCAUGGAACUACAGA 5474
5462 AAAGTTTGTAGGAGTTTCGTGTAGTAAATCCAAATCGCTGTGTGAAATCTCGAAAGTTTCC 5521
5475 AGAAGUCUGUAGUAGUUGAUGGAAGUUGCCUUAUGUCCAGCAAGGUGUCAAAGUUCG 5534
5522 GG-----AAAACAAAGAAATGTTAGTAAATGTTAATAT----- 5561
5535 AUCUCGAACCGAAAAAGAGUGAUGCCGCAAGGGAUAAUAGUAGUAAUUGAUCGUG 5594
5562 -----AAGAAAAATAATAACAGTGTGTAAGAGGGTTTTTAAATTTGAGGAAATTTGAGA 5614
5595 AGUCCCGAAACAGAAAUUAUAGAAUUAUAGGAUUUUGGAGGAUAGAUUUUAAAAAGAA 5654
5615 TAATGTAAAGTATACACAGT-----CTATCGGTATCGAGTACGTTTTTATCAAT 5665
5655 UAAUUAUUCGAUGAUGAUCGAGGCUACUGUGCCGAAUUCGGAUUCGUUUA---AAU 5711
5666 ATGCTTTATACATCAACTCTCCGAGCCAAATTTTGTACTTTATCTTCGCTTACGCAGAT 5725
5712 AUGUCUACAGUAUCACUACUCCAUUCAGUUCUGUGUUUUGCAUCAGCGUGGCCGAC 5771
5726 CCTGTGACGCTGATCAATCTGTGTACAAATGCAATTTGGTAAACCAATTTTCAACACGCAACAA 5785
5772 CCAUAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5831
5786 GCTAGGACAAACAGTCCAAACAGCAATTTGCGGATGCTGTGAAACCTGTGCTTAGTATGACA 5845
5832 GCUCGAAUCUGUGUUAAGAAACAAUUCAGUGAGGUGUGGAAACCUUACCAAGUAACU 5891
5846 GTGAGATTTCTGATCGGATTTCTATGTGTATAGATATAATTCGACGCTTGCCTGATCGTTG 5905
5892 GUUAGUUCUCCGACAGACUUAUUAAGUGUACAGGUAUUAUAGGUAUUAUAGACCCGCUA 5951
5906 ATCAGCGGTTTAAATAGCTTTGATATAAGAAATAGAAATAAGAGGTTGATATCAAA 5965
5952 GUCACAGCUGUUAAGGUGUACUACACUAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6011
5966 CCCGACCGAATACTACTGAAATCTTAAACCGACTCAGAGGTTAGACGATGCTGTA 6025
6012 CGGAACCCACGACUGCCGAAACGUUAUGAUCUACUCUAGUAGUAGACGACGCAACGGUG 6071
6026 GCTATAAGGCTTCAATCAATTAATTTGCTTAATGAACTGTTGTTGTTGTTGTTGTTGTTG 6085
6072 GCCAUAAGGAGCGCGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6131
6086 AATCAAGCAGGCTTTGAGACTGTAGTGTGACTTGTCTGACCAACCAACTCCGCTACTTAG 6145
6132 AAUCGAGCUCUUCGAGAGCUCUUCUGUUGUUGGACCUUUGGUCUCCGACCUUUAU 6191
6146 CTATT 6150
6192 CAUU 6196

RESULT 9

US-09-466-422-2

Sequence 2, Application US/09466422

Patent No. 6303779

GENERAL INFORMATION:

APPLICANT: GARGER, STEPHEN

HOLTZ, R. BARRY

MCCULLOCH, MICHAEL

TURPEN, THOMAS

TITLE OF INVENTION: A PROCESS FOR ISOLATING AND

PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES

FROM PLANT SOURCES

NUMBER OF SEQUENCES: 5

Db	2778	UUCAUUGAUGAAGGGUUGAUGUUGCAUACUGGUGUGUUAUUUUUUUGUGGCGAUGUCA	2833
Qy	2825	GGTTGCGACATCGCATACATTTCACGGAGATACACAGCAGAGATTCCTTTTCATTAAACAGAGTT	2884
Db	2838	UUGUGCGAUAUUGCAUAUUGUUUACCGAGAGACACACAGCAGAUUCCAUACAUCUAUAGAUU	2897
Qy	2885	CAGAAATTTCCGTTATCCCAACAACTTTTGAAGAGCTGCAAGTGGATGAAGTTGAGATGAGG	2944
Db	2898	UCAGGAUUCCGGUACCCCGCCCAUUUUUGCAAAUUGGAAGUUGACGAGGUGGAGACACGC	2957
Qy	2945	AGHACCACTAGAGATGCCAGGTGATGTGNAATTTTTTCTCAATCGAAGTACGAAGGA	3004
Db	2958	AGAAACUACUCUCUGGUGCCAGCGCAUGUACAACAUAUUCUGAACAGGAGAUUAGAGGC	3017
Qy	3005	GCGETGACCAACTTCAACTGTATACAGATCGGTCTCATCTGAGATGATAGCGGTAAAG	3064
Db	3018	UUUGUCAUGAGACAUCUCUCGCUUAAAGUCUCUGUUUCGCAGGAGAUUGGCGCGAGACC	3077
Qy	3065	GGAGTACTAAACAGTGTTTCCAAACCACTAAAAGGGAAAAATTGTAACTTTCACTCAGGCT	3124
Db	3078	GCCGUGACAUCUCCGAUCUCAAAACCCUUGCAGUGCAAGAUCCUGACUUAUCCCAUUCG	3137
Qy	3125	GATAAATTTGAGTTAGAGAGAGAGGGCTATAAGAAATGTGAACACCGTTCATAGATCCAA	3184
Db	3138	GAUAAAGAAGCUCUCUGCUUUAAGAGGGUUAUUCAGAUUACUGUACUCAGUGCAUGAAGUCAA	3197
Qy	3185	GGAGAAACCTTTGAAGATGTGTCGCTGGTCAGATTGACGGCAACTCCACTGACTCTGTATT	3244
Db	3198	GCGCAGACAUAUCUCUGAUGUUUCAUAGUAGGUUAAACCCCUACACAGUCUCUCCAUCAU	3257
Qy	3245	TCCAAGTCTTCCCGCATGTTTCTAGTCGCTCTGACTAGACACACAAAGAGCTTCCAATAT	3304
Db	3258	GCAGGAGACGCCCAUAUUGUUUGUCGCAUUGUACAGGCACACCTUUGCGUCUACGUAC	3317
Qy	3305	TACACCTAGTGTGATGCTTTTAGTACAGATAATTAGTGTATTGTTCTTTTAAAGTCC	3364
Db	3318	UACACUGUGUUAUGGAUCCUUUAGUUAGUAUCAUUAAGAGAUCAUGAGAAAACUUGACUG	3377
Qy	3365	TTCCTTTTTGAAGATGATATGTTAGAGCAGGTAGTAGTAGCAATTTACAGATGGAATGCA	3424
Db	3378	UACUUGUUAUUAUGUAUAGUGCGAUGCAGGAAACAUAUAGCAAAUUAACAGAUUGACUG	3437
Qy	3425	GTGTTTCAAAGTCTATAATCTCTTGTGGCAACACTTAAATCAGGAGACTTTCCAGATCTA	3484
Db	3438	GUGUUCAAAGGUUCCAAUCUUUUGUUGCAGCGCCAAAGACUGUGUAUUAUUCUGAUUG	3497
Qy	3485	CAGTTCTATTACGATGATGCTCCCTGGTAAATAGTACTATATCTATTAACAAGTATGATCT	3544
Db	3498	CAGUUUAUUAUGAUAAGUGUCUCCAGGCACACAGCACAUGAUGAAUUAUUUUGAUGCU	3557
Qy	3545	GTTACCATGAGTTACGTGATAATAGTCTTAAATGTGAAGATGTGTGTTCTTGATTTTCC	3604
Db	3558	GUUACCAUGAGGUUGACUGACAUAUUAUGAUAUGUCAAAAUUGCAUAUUGGAUUAUGUCU	3617
Qy	3605	AAAAGTATTCCGATGCCAAAGGAGGTGAAACCAATGCTCTAGAGCCAGTTTTCGCTACCGCG	3664
Db	3618	AAGUCUUGUGCGCCUUAAGGAUCAAAUCAAACCAUAUACUUAUGGUACGAAACGCGC	3677
Qy	3665	GCGGAACCGCAAGGGCTGCAGGACTACTCGAAAATCTGGTTGCAATGATTTAAAAGAAAT	3724
Db	3678	GCAGAAUUGCCACGCCAGACUGGACUAUUGGAAAAUUUAGUGGCGAUGAUUAAAAGGAAC	3737
Qy	3725	TTCAAACGACACGACCTGACGGGACGATTTGACATTCGAGAGCACCGCATCTGTGTAGTA	3784
Db	3738	UUUAACGCACCCGAGUUGUCGGCAUAUUGAUAUUGAAAAUAUCUGCAUCUUUAGUUGUA	3797
Qy	3785	GATAAGTTTTTTTGTAGTCTATTTTATTTAAAAAAGAAAAATACACAAAAATATTCTGGGA	3844
Db	3798	GAUANGUUUUUUGAUGAUUUUUUCUUAAAGAAAAAGAAAAACCAAUUAUAAAAUUGUUUCU	3857
Qy	3845	GTGATGCAAGGATTCAAATGATGAGATGGTTGGAAAAACAGGAAGAAGTACTATTGGAC	3904
Db	3858	UUUUUACUAGACAGAGUCUCUCAAUAGAUUGUUUAGAAAGCAGGAAACAGGUAAACUUAAGGC	3917

[illegible]

Db 2298 GUCUUGGAUUGCAUCUUAAGGAUGUUUAUCAAACCAACGCGCAAGAGUACAUGG 2357
Qy 2354 GGAGTTGTCCTGGATTACAAAGGGGAAATGTTTACTGCACTTCTATCTTATGAAGAGAT 2413
Db 2358 GGUUGUUGUAAACCAACCGGAGGAAGUAUCAUGUGCGCCUUUGGAUAUAGAGCAG 2417
Qy 2414 AGAATGGTGACTGAGAGCGACTGGAGAGGGTGTGTATCATCTGATACAAATGGTATAT 2473
Db 2418 GGUUGUGUGACAUGCGAUGAUGGAGAGAGAGUGUGUGCAGCUCUGAGUGUGUUUAU 2477
Qy 2474 TCTGATATTGCAAGGCTCAAATCTGAGGAAACAAATGAGAGAGCGGTGAACCCACGAA 2533
Db 2478 UCCGACUGGCGAAACUCAGAAACUCUGCGCAGACUUGUUGGAAACGAGAACCGAUGUC 2537
Qy 2534 CTTACTGCAAGATGCTCTGTGATGGGTGCTGTGTGTGGAAAGTACAAAGAGAT 2593
Db 2538 AGUAGCGCAAGGUUUCUUGAGACGAGUUCGCGGUGUGGAGAAACCAAGAAUU 2597
Qy 2594 TTTGAAAGATTTGATCTTGATGAGGATTTGATCTTTGGTTCTTGGAAACAAAGCTGCT 2653
Db 2598 CUUCCAGGCUUAUUUUGAUGAUAUUAUUUUAUACUUGGGAAGCAAGCCGCGAA 2657
Qy 2654 ATGATCAGAAAGGCTTAATCTCTGACTGATAGAGCCACCAATGACACAAATGTGAGA 2713
Db 2658 AUGAUCAGAAAGCGUGCGAAUUCUCAGGGAUUUUGUGGCCACGAGAGCAACGTUAAA 2717
Qy 2714 ACGGTAGATTCATCTTAATGATCCAAACCCGCGATCACA-----CAAGAGGCTT 2764
Db 2718 ACCGUUGAUUUUCUUGAUGAAUUUUGGGAAGACACACGCGUGUCAGUUUCAAAGAGUUA 2777
Qy 2765 TTTATTGATGAAGGGTTGATGTGCACACCGGTGTGTGTTAACTTCTGTGCTTATCTCT 2824
Db 2778 UUAUUGAUGAAGGUUGAUGUUAUCAUGUGUGUUAUUUUCUUGUGCGGAUGUCA 2837
Qy 2825 GGTGCGACATCGCATACATTTACGAGATACACAGCAGATCTCTTCAATTAACAGATT 2884
Db 2838 UUGUGGAAUUGCAUUAUUAUACGAGACACACAGCAUUAUUAUUAUUAUUAUUAU 2897
Qy 2885 CAGAAATTCCTGATCCCAACATTTGAGAGAGCTCAAGTGGATGAGTCAAGTGAAG 2944
Db 2898 UCAGAAUUCGCCUACCCGCCAUUUUGCCAAUUGGAUUGAUGAGGUGAGACACGC 2957
Qy 2945 AGGACACACTGAGATGCCAGGTGATGTGAATTTTCTTCAATCGAAGTACGAAGGA 3004
Db 2958 AGAAUUAUCUUGUUGCCGCGAUGUACAACAUUAUCUGAACAGGAGUAUGAGGCG 3017
Qy 3005 GCGGTGACAACTTCACTGTACAAAGATCGGTCTCATCTGAGATGATAGCGGTAAAG 3064
Db 3018 UUUUGAUGAGCACUUCUGGUTUAAAAGUCUUGUUCGACGAGAGUUGUGCGGAGCC 3077
Qy 3065 GGAGTACTAAACAGTGTTCCTAAACCACTAAAGGGAAATTTGTAATCTTCACTCAGGCT 3124
Db 3078 GCGGUAUUAUCCGUAUCUAAACCCUUGCAUGGCAUGAUCUGAUUUUUAACCAUUGC 3137
Qy 3125 GATAAATTTGAGTTAGAGAGAGGCTATAGAATGTGAACACCGCTTCATGAGATCCAA 3184
Db 3138 GAUAAAGAAGCUCUGCUUAACAGAGGUAUUAUGAUGUUAUUAUUAUUAUUAUUAU 3197
Qy 3185 GGAGAAACCTTTGAAGATGTGTGCTGCTGATGACGGCAACTCCACTGATCTGTATT 3244
Db 3198 GCGGAGACAUACUCUGAUGUUUACUAGUUAAGUUAACCCUACACACAGUUCUUAU 3257
Qy 3245 TCCAGTCTTCCCGGATGTTCTAGTCGCTCTGACTAGACACAAAGAGCTTCAATAT 3304
Db 3258 GCAGGAGACAGGCCCAUGUUUGUGCAUUGUUAAGGACACACUUGUGCUCAAGUAC 3317
Qy 3305 TACACGCTAGTGTAGATCTTTAGTACAGATAATTTAGTGTATTGTCTTCTTAAGCTCC 3364
Db 3318 UACAUUGUUAUUAAGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUG 3377
Qy 3365 TTTCTTTTGAAGATGTATGTTAGAGAGGAGTGTATGATAGCAATTTACAGATGGATGA 3424
Db 3378 UACUUGUUAUUAUUAAGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUG 3437
Qy 3425 GTTTTCAAAGGTCATAATCTCTTTGTGGCAACACCTAAATCAGGAGACTTTTCCAGATCTA 3484
Db 3438 GUGUUAAGGUGUCCAAUUCUUUUGUGCAGCGCCAAAGAGUGGUGAUAUUUCUGAUAUG 3497
Qy 3485 CAGTTCTATTACGATGTATGCTCCTCTGTATAGTACTATATACTTAAACAAGTATGATGCT 3544
Db 3498 CAGUUUAUCAUGAUAAGUGUCUCCAGGCAACAGCACCAUGAUAUAUUUUGAUAUG 3557
Qy 3545 GTTACATGAGGTTACGTGATAATAGTCTTATGTGAAGGATGTGTCTTCTGATTTTTCC 3604
Db 3558 GUUACCAUGAGUGUACUGACAUUUAUGAUGUCAAAGAUUGCAUAUUGAUAUGUUAUGUCU 3617
Qy 3605 AAAAGTATTCGATGCCAAAGAGGTGAAACCATCTCTAGAGCCAGTTTGTGCTACCGCG 3664
Db 3618 AAGUCUGUGUGCGCCUAGGAUCAAUCAAACCAUAAUACCUAUGGUAACGAAACGCG 3677
Qy 3665 GCGGAACCGCCNAGGGCTGCAGGACTACTCGAANAATCTGGTTGCAATGATTAAGAAAT 3724
Db 3678 GCAGAAUUGCCACGCGCAGACUGGACUUAUGGAAAUUAUGGCGCAUGAUAUAAAGGAAC 3737
Qy 3725 TTCAACGACACAGACTGACGGGACGATTGACATTTGAGAGCACCGCATCTCTGTGTATGA 3784
Db 3738 UUUAAAGCACCGAGUGUGUGCAUUAUGAUAUUGAUAUUGAUAUUGCAUUAUUGAUAUG 3797
Qy 3785 GATAAGTTTTTTGATGATCTTTTATTAATAAAGAAATAACAAAAAATATTTGCTGGA 3844
Db 3798 GAUAAUUUUUUGAUAUUAUUUUAAGAAAGAAAGAAACCAAAUAAAUAAUUGUUUCU 3857
Qy 3845 GTGATGACGAAGGATTAATGATGATGTTGTTGAAACACAGAAAGAGTACTATTTGGAC 3904
Db 3858 UUGUUCAGUAGAGAGUCUCUCAAUAGUGGUUAGAAAGACAGAAACAGGUAAACAAUAGC 3917
Qy 3905 GACTTGGCTTAACATACTACAGATCTCGCGGCATCGATCAGTACAGACACATGATC 3964
Db 3918 CAGCUGCGAGAUUUUGAUAUUUGUUAUUUGCCAGCAUUAUGAUAUUAUGAUAUUAUG 3977
Qy 3965 AAGGCTCAACCAAAACAGAAATTTGACCTTTCAATTCAGAATGAATACCTCTCTGCAA 4024
Db 3978 AAAGCACAAACCCAAAGCAAAAUUGGACACUCAAUCCAAACGAGAGUACCGGCUUGCAG 4037
Qy 4025 ACAATTTGCTACCATTCGAAGCAGATCAACGGTATTTTGGCCGGTTCT--CAGAGCTT 4081
Db 4038 ACGAUUGUGUACCAUUAAGAAAGCAUUAUGCAUUAUUGGCGCGUUGUUAUGAGAGCU 4097
Qy 4082 ACAAGTTGCTGCTCGAGGCATTTCATCTAAGAAAGTTTCTTTCTTACTAGGAAACT 4141
Db 4098 ACUAGGCAUUAUCUGACAGUUGUUAUUGGACAGAUUUUUUUUUUUAUUAUUAUUAU 4157
Qy 4142 CCAGAACAGATTCAGAAATTTTTCGGATCTCGACTCGACCTCTTCTATGGATGTGTTA 4201
Db 4158 CCAGCGCAGAUUGAGAUUUUUCGAGAUUUCGACAGUUAUGUGCGAGUUGUUAUG 4217
Qy 4202 GAACTGGATATTTTAAAGTATGATGAAGTACAGAACGAGTTTCTGCTCTGATGATAT 4261
Db 4218 GAGCUGAUAUUAUCAAUAUACGCAAAUUCAGAAUAGUUAUUAUUAUUAUUAUUAU 4277
Qy 4262 GAAATATGGAAGAAGTTGGTCTCAATGATTTTGGCCGAAGTGTGGAACCAAGGCGAC 4321
Db 4278 GAGAUUGCGGAAGAUUGGUAUUAAGACAUUUUGGGAAGAUUUUGAUAUUAUUAUUAU 4337
Qy 4322 AGGAAAAAACAATCTGAAGGATTACATTTGCTGGAATCAAGACATGTCTGTGATCAAGG 4381
Db 4338 AGAAGAACCAACCCUACAGGAUUAUUAACCGAGUAUUAUUAUUAUUAUUAUUAUUAU 4397
Qy 4382 AAAAGCGGTGATGATCTATCTTTTCAATCGCAATATCTGTTATATAGCAGCTTGTGGGT 4441
Db 4398 AAGAGCGGGACGUCACGACGUUAUUGGAAACACUGUGAUAUUAUUAUUAUUAUUAU 4457
Qy 4442 TCAATGTTACCGATGGAAGAAGTATGAAGGTTGTTTTTGGAGACGATTCGCTTTTG 4501
Db 4458 UCGAUGCUUCCGAGGAAAAUUAUAAAGGAGCCUUUUGCGGUGACGAUAUGUCUG 4517

Db	1818	UUGAAAGUAGCCCAUUGACGGCAGCGAAAGGUUAUAGUCGCGUACAUGACCAUAGAGACG	1877
Qy	1880	GGTTTAATCTTACTTTTGTATAGCCAAACGAGGAGAAATGTGGCTTAAGGCTCT- - - - -T	1933
Db	1878	GGUCUGACUCUCAUUGAACACGACUACUGAGGCGAAUGUUGCGCUAGCUUACAGGAU	1937
Qy	1934	AAAAGCAGCGGCTGTAGGCGGTGGTATGTCTTGAACCGACATCCGAAGAGGTTGAACGTA	1993
Db	1938	CAAGAGAAGGCUUCAGAGAAGGUGCUUUGGUAGUUAUCCUACAGAGAAGUUGAAGAACCGUCC	1997
Qy	1994	AATFAATTTTCTATTGCTGAGAAAGGAGATTGCTGTGTGTGTCAGAAAAGTCATGTTTG	2053
Db	1998	AUGAAGGUGUUGAUGGCGCAGAGGAGUTUAACAUAUCUGUGUCUUGCUGAGAUCAUCCG	2057
Qy	2054	ACGAATCTTAACCTTAGAGACACGAGGTGTGAGTCCCTCAACGANTTCCATAAGGCTTGC	2113
Db	2058	GAGUCGUCCUUAUUCUAAAGAACGAGGAGUAGAGUUAUUGAGAGAGUUAUUGGCAACG	2117
Qy	2114	GTGGATAGTGTGATTACAAAGCAAAATGGCATCGGTGTCTACACTGCTCAGTCAAGATT	2173
Db	2118	GCAGAUUGUUAUUCGUAGACGAGAGUCUAGAUUGUAGUACACGGGUCGUAUAAAGUU	2177
Qy	2174	CAACAAATGAAGAACTATGTGGACAGTTTGGCAGCTTCTGTTGTCGCGCATGTATCAAAAT	2233
Db	2178	CAGCAAAUGAAAAACUUUAUCCGAVAGCUGUGAGCAUCAUAUCUGCUGCGUGUCGAU	2237
Qy	2234	CTATGCAAGTCACCTAAAGGATGAAGTCGGGTATGATTTCTGATTTCCAGGAGAAAGTTGGT	2293
Db	2238	CUCGUCAGAUCCUCAAAGAUACAGCUGCUUAUUGACCUUGAAACCCGCUAAAAGUUGGA	2297
Qy	2294	GTTTGGGATGTCACTTTGAAAAAGTGGCTCCTCAAACCTCGCGGCCAAAGGTCAATTCATGG	2353
Db	2298	GUCUGAGUUGCAUCUAGGAAGUGGUUAUACAACCAACGGCCAGAGUAGCAUGCAUGG	2357
Qy	2354	GGAGTTGTCCTGGATTACAAAGGGGAAATGTTTACTGCACTTCTATCTTATGAAGAGAT	2413
Db	2358	GGUGUGUGUAGAAACCCAGCGAGGAAGUUAUCAUGUGGCGCUUUGGAAUAUGAUGAGCAG	2417
Qy	2414	AGAATGTGACTGAGAGCGACTGAGAGAGGGTGGCTGTATCATCTGATATCAATGGTATAT	2473
Db	2418	GGUGUGUGUAGAUUGGGAAGAGUAGUCUGUCAGCUCUGAGUCUGUUGUUUUUU	2477
Qy	2474	TCTGATATTGCAAAAGCTCCAAAATCTGAGGAAAAACAATGAGAGACGCGTGAACCCACGAA	2533
Db	2478	UCCGACAUUGCGAAACUCAGAAACUCUGCGCAGACUGCUUGAAACGGAGAACCGCAUGUC	2537
Qy	2534	CCTACTGCAAGATGGTACTTTGTGGATGGGTGGCTGGTTGTGGAAGTACAAAGAGAT	2593
Db	2538	AGUAGCGCAAAGGUUUCUUGUGGACGAGUUCGCGGCUUGUGGGAAGAAACCAAGAAAUU	2597
Qy	2594	TTTGAAAGATTGATCTTGATGAGGATTTGATCTTGGTTCTTGGAACCAAGCTGCTGCT	2653
Db	2598	CUUUCGAGGUUAUUUGAAGAGUACUAAUUUUGUACUGGGAAGCAAGCGCGGAA	2657
Qy	2654	ATGATCAGAGAAGGGCTAATTCACTCGGACTGATAAGAGCCAATGCAATGTGAGA	2713
Db	2658	AUGAUCAGAGACGUGGNAUUUCUAGGGAUUAUUGUGGCCACGAGAGACACGCUUAAA	2717
Qy	2714	ACGGTAGATTCACTTCTAATGATCCAAAACCGCGATCACA- - - - -CAAGAGGCTT	2764
Db	2718	ACCGUGAUUUCUUAUGAUGAAUUUUGGGAAGAACACACGUCUGAGUUAUACAGAGGUUA	2777
Qy	2765	TTTATTGATGAAGGGTTGATGCTGCACACCGGTTGTGTTAACTTCCTCGTGGCTTATCTCT	2824
Db	2778	UUAUUGAUGAAGGGUUGUUGGCAUACUGGUGUGUUAUUUUUUGUGGCAUGUCA	2837
Qy	2825	GTTTGGCAGATCGCATACATTTACGGAGATACACAGCAGATTCTCTTTCAATTAACAGAGTT	2884
Db	2838	UUGUGCGAAUUAUGCAUUGUUUACGGAGACACACAGCAGAUUCCAUACAUACUAGAGUU	2897
Qy	2885	CAGAAATTTCCGTTATCCCAACATTTTTGAGAAGCTGCAAGTGGATGAAGTTGAGATGAGG	2944

2998	UCAGGAUUCCGUACCCCGCCCAUUIUGCCAAAUUGGAAGUACGAGGUGGAGACACGC	2995
2945	AGGACCACTGAGATGCCAGGTGATGTGAATTTTTTCTCAATCGAAGTACGAAGGA	3004
2958	AGAAUACUACUCUGUUGUCCAGCGCAUGUACACAUAUUCUGAAACAGGAGUAUAGAGGC	3017
3005	CGGTGACAACCACTTCACTGTACAACGATCGGTCTCATCTGAGATGATAGGGGTAA	3064
3018	UUUGUCAUGAGCACUUCUCGGUUA AAAAGUCUGUUIUCGAGGAGUUGUCGGCGAGCC	3077
3065	GGAGTCTAAACAGTGTTCACAAACCACTAAAAGGGGAAAATTGTAACTTTTCACTCAGGCT	3124
3078	GCCGUGAUCAAUCGGAUCCUCAAACCCUUGCAUGGCAAGAUCCUGACUUUUACCAUUG	3137
3125	GATAAAATTTGAGTTAGAGGAGAAAGGGCTATAAGAAATGTGAACACCGCTTCATGAGATCCAA	3184
3138	GAUAAAGAAGCUCUCUUAACAGAGGUAUUCAGAUGUACACUCUGGCAUGAAGUGCAA	3197
3185	GGAGAAACCTTTGAAAGATGTGTCGTGTCAGATTGACGGCAACTCACTGACTCTGTGATT	3244
3198	GGCGAGACAUAUCUGAUGUUUACUAGUUAAGGUUAACCCCUACACCAUGUCUCCAUCAUU	3257
3245	TCCAAGTCTTCCCGCATGTTCTAGTCGCTCTGACTAGACACACAAAGAGCTTCAAAATAT	3304
3258	GCAGGAGACAGCCCAUGUUUUUGUGCGCAUGUGUCAAAGGCACACCUUUCGCUCAAGUAC	3317
3305	TACACCGTAGTGTAGATCCTTTAGTACAGATAATTAGTGAATTTGTCTCTTTAAAGTCCTC	3364
3318	UACACUUGUUUAUGGAUCCUUUAUUAUUAUACUAUAGAGAUUCUAGAGAAACUUAGCUCG	3377
3365	TTCTCTTTTGAATGTATGTGTAAGACAGGTAGTGTAGTAGCAATTTACAGATGGATGCA	3424
3378	UAUUGUUAGAUUAUAAAGGUCGAUGCAGGAAACAUAUAGCAAAUACAGAUUGACUCG	3437
3425	GTGTTCAAAGGTCAATATCTTTTGTGGCAACACCTTAAATCAGSAGACTTTCAGAGTCTA	3484
3438	GUGUUCAAAGGUUCCAAUCUUUUUUGUGCGCAGCGCAAAGACUGGUGHAUUAUUGUAUUG	3497
3485	CAGTTCTATTACGATGTATGCTCCCTCGTGAATAGTACTATCTTAAACAAGTATGATGCT	3544
3498	CAGUUUAUAUAGUAAGUCUCCACGAGCAACAGCACCAUGAUGAUAUUUUAUGUCU	3557
3545	GTTACCATGAGGTAACTGTGAATAATAGTCTTAAATGTGTAAGGATGTGTCTTTGATTTTCC	3604
3558	GUUACCAUGAGGUUGACUGACAUAUUAUGAUAUGUCAAAGAUUGCAUAUUGGAUAUUGUCU	3617
3605	AAAAGTATTCGGATGCCAAGAGGAGTGAACCATGTCTAGACGCAGTGTTCGCTACCGCG	3664
3618	AAGUCUGUUGCUGCGCCUUAAGGAUCAAAUACCAACCUAAUACCUAUGGUCAGAACCGCG	3677
3665	GCGAAACGCAAGGGCTCAGGACTACTCGAAAAATCTGGTGTCAATGATTTAAAGAATAAT	3724
3678	GCAGAAUGCCA CGCAGACUGGACUAUUGAAAAUUUUGGCGGAUGAUUAAAAGGAAC	3737
3725	TTCAACGCAACAGACCTGACGGGAGCAGATTGACATTTGAGAGCACCGCATCTGTTGTAGTA	3784
3738	UUUAAACGACCCGAGUUGUCUGGCAUCAUUGAUUUGAAAAUAUCUGCAUCUUUUAUGUUA	3797
3785	GATTAAGTTTTTTGATACCTATTTTATTTAAAAAGAAAAATACACAAAAATATTTGCTGGA	3844
3798	GAUAAGUUUUUUGAUGAUUAUUGUUAAGAAAAAGAAAAACCAAUAAAAUUUUUUUU	3857
3845	GTGATGACAGAGGATTCAAATGATGAGATGGTGGAAAAACAGGAAGAAGTACTATTGGAAC	3904
3858	UUGUUCAGUAGAGAGUCUCUACUAUGAUGGUUAUAAAAAGCAGGACAGGUACAUAUAGGC	3917
3905	GACTTTGGCTAACTACAAATTTTACAGATCTCGCGGCCATCGATCATGTAACAAGCATGATC	3964
3918	CAGCUCGAGAUUUUGAUUUUUGAUUUUGCAGCAGUUAUUGCAUACAGUACAUAUUA	3977
3965	AAGGCTCAACCAACAGAAATTTGGACCTTTCAATTCAGATGAATACCTCGTCTCAAA	4024
3978	AAAGCAACACCCAGCAAAAAUUUGGACAUUUUUAUCCAAACCGAGUACCCCUUUGCAG	4037

3018 UUUUGAUGAGCACUUUCUGGUUAAAAAAGUCUGUUUCGACGAGAUUGUGCGGCGAGCC 3077
3065 GGAGTACTAAACAGTGTTCACAAACACCTAAAGGAAATTTGTAATTTTCACTCAGGCT 3124
3078 GCGGUAUCAAUCCGAGUCCUAAAACCCUUGCAUGGCAAGUCCUAGCUUUUAACCAUCC 3137
3125 GATAAATTTGAGTTAGAGGAGGAGGCTATAAGAAATGTGAACACCGTTTCATGAGATCCAA 3184
3138 GAUAAAGAGCUCUGCUUUAAGAGGGUUAUCAGAUUGUUCACACUGUGCAUGAAGUGCAA 3197
3185 GGAGAAACCTTTGAAGATGTGTCGTGTCAGATTGACGGCAACTCCACTGACTCTGATT 3244
3198 GCGGAGACAUACUCUGUUGUUCACUAGUUGUUAACCCUACACCGAGUCUCCAUCAU 3257
3245 TCCAAAGTCTTCCCGCATGTTCTAGTCGCTCTGACTAGACACACAAAGAGCTTCAAAATAT 3304
3258 GCAGAGACAGCCCAUUGUUUGUGGCAUUGUUCAGGCAACACUUGUCCUGCAUAGUAC 3317
3305 TACACCGTAGTGTAGATCTTTAGTACAGATAAATTTAGTGAATTTGTCTTTTAAAGTCC 3364
3318 UACACUGUUGUUAUGAUCUUAUGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3377
3365 TTCTCTTTAGAAATGTATAGTAGAAGCAGGTAGTAGATGAGCAATTAAGATGATGCA 3424
3378 UACUUGUUAUUAUUAUUAAGGUCGAGCAGGAAACACAAUAGCAAUUAACAGAUUGACUG 3437
3425 GTGTTCAAGGTCAATCTCTTTGTGGCAACACCTAAATCAGGAGACTTCCAGATCTA 3484
3438 GUGUUCAAAGGUGUCCAAUUCUUUGUGCAGCGCCAAAGACUGGUGUAUUAUUCUGAUUG 3497
3485 CAGTTCATTTAGCATGTATGCTCTCCCTGCTGTAATAGTACTATCTTTAAACAAGTATGATCT 3544
3498 CAGUUAUUAUUAUUAUGAUGUUCUCCAGGCAACAGCACCAGUAGAAUUAUUAUUAUGCU 3557
3545 GTTACATCAGGTTACGTGATATAGTCTTAATGTGAAGATTTGTTCTTGAATTTTCC 3604
3558 GUUAACUAGAGGUGACUGACAUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3617
3605 AAAAGTATTCGATGCCAAGAGGTTGAACCACTGCTAGACCAAGTGTTCGTGTCGCG 3664
3618 AAGUCUGUGUGCGUCCUAAAGGAUCAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3677
3665 GCGGAACCCGCAAGGCTGACGAGTACTCGAAATCTGTTGCAATGATTAAGAAAT 3724
3678 GCAGAAUCCAGCCGACAGACUGACUUAUUGAAAUUAUUAUGGCGCAUUAUUAAGAAAC 3737
3725 TTCAACGCAACGACCTGACGCGGACGATTTGATTTGAGAGCACCGCATCTGTTGATGA 3784
3738 UUUUACGCAACCCGAGUUGUGUGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3797
3785 GATAAGTATTTGATAGCTATTTTAAAGAAAGAAATACACAAATAATTTGCTGGA 3844
3798 GAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3857
3845 GTGATCAGCAAGGATTTCAATGATGATGTTTGAAGAAACAGGAAGAAGTACTATTGGAC 3904
3858 UUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3917
3905 GACTTGGCTTAACATAATTTTACAGATCTCGCGCCATCGATCAGTACAGCAATGATC 3964
3918 CAGCUCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3977
3965 AGGCTCAACCAAAACAGAAATTTGAGCTTTTCAATTCAGATGAATACCTGCTGCGAA 4024
3978 AAAGCAACACCCAAAGCAAAUUGGACAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4037
4025 ACAATGTCTTACCATTTGAGCAGATCAACGGTATTTTGGCCGCTTCT---CAGAGCTT 4081
4038 ACAGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4097
4082 ACAAGGTGCTGCTCGAGGCAATTTGATTTCTTAAGAGTTCCTTTTCTTACTAGGAAACT 4141
4098 ACUAGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4157

4142 CCAGAACAGATTTCAAGAAATTTTCTCGATCTCGACTCGCAGTTCCTATGATGTGTTA 4201
4158 CCAGCGCAGAUUUGAGGAUUAUUCGGAUUAUUCGACAGUAGUGCCGAGUAGUUCUUG 4217
4202 GAACTGGATATTTCTAAGTATGATAGTACAGAACGAGTTTCTATTGTGCTCTAGATAT 4261
4218 GAGCUGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4277
4262 GAAATATCGAAAGAAATTTGGTCTCAATGAGTATTTTGGCGAAGTGTGAAACAAAGGCA 4321
4278 GAGAUUCGCGAAGAUUGGUUUUGAAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4337
4322 AGGAAAAACAATTTGAAGATTTACATTTGCTGGAATCAAGACATGCTGTGTGATCAAAG 4381
4338 AGAAAGACCAACCCUACAGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4397
4382 AAAAGCGGTGATGATCTACTTTCATCGCCTATCTGTTATATAGCAGCTTCTGCTGGT 4441
4398 AAGACGCGGAGCAGCAGCAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4457
4442 TCAATGTTTACGATCGAAAGGTATATAAGGTGCTTTTGTGAGACGATTTCCGTTTGG 4501
4458 UCGAUGCUUCCGAGGAGAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4517
4502 TATTTTCCAAAGGTTTGGATTTCCCTGACATTTCACTCATGTGCTTAATCTCATGTGGAAT 4561
4518 UACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4577
4562 TTTGAGGCGCAAACTGTATAGAAAGGTACGTTTACTTTTGTGTTAGATACATCATAC 4621
4578 UUUUAGCAAAACUGUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4637
4622 CATGATAAGGAGCAATAGTATGATCTCTTGAAGTCTCTTCAAACTTGGGCA 4681
4638 CAGACAGAGGAUGAUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4697
4682 AAAACATCAAGGATTTATGATCACTTAGAAGATTAAGGTTGCTTTTGTGCGATGTGCT 4741
4698 AAAACAUCAAGGAUUGGAAACACUUGGAGGAGUUAUUAUUAUUAUUAUUAUUAUUA 4757
4742 TTTTCTCGTCCGAAACTGTGTCTTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCG 4801
4758 GUUUCUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4814
4802 CATAAAAACCGGATTTGATGTTGCTTTGCTTTTAAATTTGTTAAACAAATTTTGTGAT 4861
4815 CAUAAAGACCGCCGCCUCCAGGUUGUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4874
4862 AAATTTTATTTAGAACTTTGTTTTTAAATGCTGTTAGTCTCAGAGATACCTGTCAAAT 4921
4875 AAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4934
4922 TAGCAGATTCATGATCTTTTGAACACAGGATGAGTACTTTCCGGCATTTCTGATCAAG 4981
4935 CAUAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4994
4982 CAGAGTGTAGAAATATCGACTGTGAGCAAGATTTAGGCTGTTTAAAGATGATGTTCTTC 5041
4995 AAAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5054
5042 TGATGTAGATTTTACTTTAAAGGTGTTTAAAGTGTAGTTAAGAAAGGATGTTGTGCTAG 5101
5055 AGAGGUAACCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5114
5102 TTTGTTAGTGTCTGGGAGTGGAACTCCCGGATACTCCCGGATGCTGCTGCTGCTGCTG 5161
5115 UUUUGGUGCAACGGGCGAGUGGAAACUUGCCUGACAAUUAUUAUUAUUAUUAUUAUUA 5174
5162 TATTGTAGATAGAGATGAAAGGATTAAGGAAGCAACGCTGGGTGCTGCTGCTGCTGCT 5221
5175 UCUUGGUGGCAAAAGGAUUAAGAGCCGACGAGGCGCACUUGCGGAUUAUUAUUAUUA 5234

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 28, 2005, 08:33:34 ; Search time 2408.02 Seconds
(without alignments)
17081.170 Million cell updates/sec

Title: US-09-551-494-5
Perfect score: 6355
Sequence: 1 gatgttttaataagtttttcga.....taaccgcggtagcgccca 6355

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues 14575566
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
8: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6355	100.0	6355	15	US-10-321-434-7
2	2468	38.8	6395	10	US-09-962-527-1
3	2468	38.8	6395	19	US-10-828-029-1
4	2466.4	38.8	6395	17	US-10-338-592-2
5	2455.4	38.6	6439	10	US-09-962-527-2
6	2455.4	38.6	6439	19	US-10-828-029-2
7	2452.2	38.6	6475	10	US-09-962-527-4

ALIGNMENTS

RESULT 1

US-10-321-434-7
; Sequence 7, Application US/10321434
; Publication No. US20030135882A1
; GENERAL INFORMATION:
; APPLICANT: Metzlaff, Michael
; APPLICANT: Meulewater, Frank
; APPLICANT: Gossel, Veronique
; APPLICANT: Fach, Ina
; TITLE OF INVENTION: Improved methods and means for delivering inhibitory RNA to plants
; FILE REFERENCE: PROMOD
; CURRENT APPLICATION NUMBER: US/10/321,434
; CURRENT FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 6355
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: cdna sequence of the genome of TMV-U2
US-10-321-434-7

Query Match 100.0%; Score 6355; DB 15; Length 6355;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATGTTTAAATAGTTTTCGACAAACAATTAACAAACAAACATATTACAAACA 60
|||||

Sequence 4, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 73, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 22, Appli
Sequence 25, Appli
Sequence 25, Appli
Sequence 25, Appli
Sequence 22, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 24, Appli
Sequence 24, Appli
Sequence 24, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli

Db 1 GATGTTTAAATAGTATTTTCGACAAACAATTAATAAACAACAAACATATTACAAACAACA 60
Qy 61 AACAAACAATAGGCACACATACAAATCTATATTAATAGCAACGCCCTTCTTGAAACGGTGAG 120
Db 61 AACAAACAATAGGCACACATACAAATCTATATTAATAGCAACGCCCTTCTTGAAACGGTGAG 120
Qy 121 TGGTAAAAAACHACTCTCGTTAATGACCTTGCAGAAAGGGGCATGTACGATACGGCCGTGGA 180
Db 121 TGGTAAAAAACHACTCTCGTTAATGACCTTGCAGAAAGGGGCATGTACGATACGGCCGTGGA 180
Qy 181 AGAATTTAAACCCCGCAGCCGTAGACCAAGAGTCAACTTTTCCAAAACATATTACGGAAGA 240
Db 181 AGAATTTAAACCCCGCAGCCGTAGACCAAGAGTCAACTTTTCCAAAACATATTACGGAAGA 240
Qy 241 GCAAAACGCTTCTAGTCTCCAAACGGGTACCCGGAGTTCAGATTAACCTTTTATATACTCA 300
Db 241 GCAAAACGCTTCTAGTCTCCAAACGGGTACCCGGAGTTCAGATTAACCTTTTATATACTCA 300
Qy 301 AAATGCCGTACACAGTTTGGCTGGAGTTTGAGAGCAATTAGAAATGGAATATCTGATGCT 360
Db 301 AAATGCCGTACACAGTTTGGCTGGAGTTTGAGAGCAATTAGAAATGGAATATCTGATGCT 360
Qy 361 ACAAGTTCCCTATCGATCGCCGACATATGATATAGTGGGAACCTTGCAGCACATTTGTT 420
Db 361 ACAAGTTCCCTATCGATCGCCGACATATGATATAGTGGGAACCTTGCAGCACATTTGTT 420
Qy 421 CAAAGCAGGAGTATACGTCGATTCGTGATGCCCAATCTGGACATACGAGATATAATGAG 480
Db 421 CAAAGCAGGAGTATACGTCGATTCGTGATGCCCAATCTGGACATACGAGATATAATGAG 480
Qy 481 GCACGAGGACAAAGAGCTCAATGAGATGTATTTGTCAGATGTCTCGTTCATAACAA 540
Db 481 GCACGAGGACAAAGAGCTCAATGAGATGTATTTGTCAGATGTCTCGTTCATAACAA 540
Qy 541 GGTAAATCTCAGTTTCAAAGGGAGGCTTTTAAACAGGTATGCAGAGCTCCCAACGAGT 600
Db 541 GGTAAATCTCAGTTTCAAAGGGAGGCTTTTAAACAGGTATGCAGAGCTCCCAACGAGT 600
Qy 601 CTGCTGCTCTAAAACTTTTCAGGATGTCGAATACATCCCGCAGAGAATAGTGGTAGAG 660
Db 601 CTGCTGCTCTAAAACTTTTCAGGATGTCGAATACATCCCGCAGAGAATAGTGGTAGAG 660
Qy 661 ATAGCGTTGCTCTGCACAGTTTGTATGATATTTCTGTGTCATGAGTTGAGCTGCGTT 720
Db 661 ATAGCGTTGCTCTGCACAGTTTGTATGATATTTCTGTGTCATGAGTTGAGCTGCGTT 720
Qy 721 AATATCTAAGAAATACATGATGTATGTCAGCTTCCATTTTGGCAGAGCATTTACT 780
Db 721 AATATCTAAGAAATACATGATGTATGTCAGCTTCCATTTTGGCAGAGCATTTACT 780
Qy 781 AGACGACGAGGTTTACGCTTAATGAATAGGCGCAACTTTCAAAGAGAGGTTGATGA 840
Db 781 AGACGACGAGGTTTACGCTTAATGAATAGGCGCAACTTTCAAAGAGAGGTTGATGA 840
Qy 841 TGTTCCTTTTCTTGTGTCATGAAGTACCTTTAAATTTATAGTCATATAACAAAATAT 900
Db 841 TGTTCCTTTTCTTGTGTCATGAAGTACCTTTAAATTTATAGTCATATAACAAAATAT 900
Qy 901 CTTGCATTTATGTTAAATCTTACTTTCCTGCTCTAGTAGAATAGTTTACTTTAAGGA 960
Db 901 CTTGCATTTATGTTAAATCTTACTTTCCTGCTCTAGTAGAATAGTTTACTTTAAGGA 960
Qy 961 ATTTTATGCTACAGGGTAAATCTTGGTTTGTAAATTTTACAAAGTAGATACCTATAT 1020
Db 961 ATTTTATGCTACAGGGTAAATCTTGGTTTGTAAATTTTACAAAGTAGATACCTATAT 1020
Qy 1021 TCTGTACAAGAGTGTAGACAGTAGGTGTAGTATGATCAGTCTCTATGAGGCGATGA 1080
Db 1021 TCTGTACAAGAGTGTAGACAGTAGGTGTAGTATGATCAGTCTCTATGAGGCGATGA 1080
Qy 1081 AGAGCCCTTTGCTTACAGAAAAA CTTTGGCCATGTTTCAACACTGAAAGAGCAATCTTTAG 1140
Db 1081 AGAGCCCTTTGCTTACAGAAAAA CTTTGGCCATGTTTCAACACTGAAAGAGCAATCTTTAG 1140

Qy 1141 AGACACGGCTTCGGTTAACTTTTGGTTCCCTAAGATGAAGACATGTGTGATAGTACCGCT 1200
Db 1141 AGACACGGCTTCGGTTAACTTTTGGTTCCCTAAGATGAAGACATGTGTGATAGTACCGCT 1200
Qy 1201 GTTTGAGGGTTCATTATACAGCAAAAGATGACAAGGAGTGAGTCAATTGTTAATCGTGA 1260
Db 1201 GTTTGAGGGTTCATTATACAGCAAAAGATGACAAGGAGTGAGTCAATTGTTAATCGTGA 1260
Qy 1261 CTTTCGTTTTACACAGTGTCTAATCATATCAGAACATATCAAGCCCAAGCGTTAACTTACCA 1320
Db 1261 CTTTCGTTTTACACAGTGTCTAATCATATCAGAACATATCAAGCCCAAGCGTTAACTTACCA 1320
Qy 1321 GAAAGTATTAATCTTTTCGTGAGTCTATAAGATCCCGGTGATATAATCAATGGTGTACTGC 1380
Db 1321 GAAAGTATTAATCTTTTCGTGAGTCTATAAGATCCCGGTGATATAATCAATGGTGTACTGC 1380
Qy 1381 TAGGTCTGAATGGGATGTAGATAAGCAATTTCTTCAACCCCTTGTCAATGACTTTCTTCTT 1440
Db 1381 TAGGTCTGAATGGGATGTAGATAAGCAATTTCTTCAACCCCTTGTCAATGACTTTCTTCTT 1440
Qy 1441 GCAGACTAAGCTGGCTGCTTCAAGACGATATAGTAATGGGAAAGTTTCGGTCTTGGGA 1500
Db 1441 GCAGACTAAGCTGGCTGCTTCAAGACGATATAGTAATGGGAAAGTTTCGGTCTTGGGA 1500
Qy 1501 TAAGACCACTTCTGAACTTATTTGGGATGAGTGGGCAAAATTTTTCGAAAACGTTTCCC 1560
Db 1501 TAAGACCACTTCTGAACTTATTTGGGATGAGTGGGCAAAATTTTTCGAAAACGTTTCCC 1560
Qy 1561 CACTATCAAAAGAGAGATTGGTGAGCAGGAAATTTCTGGATGTAAAGTGAAGATGCTCTGAA 1620
Db 1561 CACTATCAAAAGAGAGATTGGTGAGCAGGAAATTTCTGGATGTAAAGTGAAGATGCTCTGAA 1620
Qy 1621 GATCAAGATCCCAGATCTGTATGTGCATGCGAAAGCAGAGTTTCGTAGCTGAATACACCA 1680
Db 1621 GATCAAGATCCCAGATCTGTATGTGCATGCGAAAGCAGAGTTTCGTAGCTGAATACACCA 1680
Qy 1681 GTCTGAGGAGTTACCGCATCTAGATATCAAGAGAGACTTAGAAGAGCTGAGCAAAATGTA 1740
Db 1681 GTCTGAGGAGTTACCGCATCTAGATATCAAGAGAGACTTAGAAGAGCTGAGCAAAATGTA 1740
Qy 1741 CGACGGTTATCAGAAATTTCTATCTTAAAGGTGCTGATAATTTTCGATATCGCGAAGTT 1800
Db 1741 CGACGGTTATCAGAAATTTCTATCTTAAAGGTGCTGATAATTTTCGATATCGCGAAGTT 1800
Qy 1801 CAAAGACATGTGCAAGGCTTTAGATGTTAGTCTCTGATGTGCGCAGCAGAGTAAATCGTTGC 1860
Db 1801 CAAAGACATGTGCAAGGCTTTAGATGTTAGTCTCTGATGTGCGCAGCAGAGTAAATCGTTGC 1860
Qy 1861 AGTGGCCGAGATAGAAAGCGGTTTAACTCTTACTTTTGAATAAGCCACCGAGGAGAATGT 1920
Db 1861 AGTGGCCGAGATAGAAAGCGGTTTAACTCTTACTTTTGAATAAGCCACCGAGGAGAATGT 1920
Qy 1921 GGCTTAAGGCTTTAAAGACACGCGCTGAGGCGGTGATGCTTGAACCGACATCCGA 1980
Db 1921 GGCTTAAGGCTTTAAAGACACGCGCTGAGGCGGTGATGCTTGAACCGACATCCGA 1980
Qy 1981 AGAGGTGAACGTAATAAATTTTCTATTGCTGAGAAAGGAGATTTGCTGTGTGCGAGA 2040
Db 1981 AGAGGTGAACGTAATAAATTTTCTATTGCTGAGAAAGGAGATTTGCTGTGTGCGAGA 2040
Qy 2041 AAGTCATGGTTGACGAATGCTAACTTTAGACCACGAGGTTGGAGTCCCTCAACGATTTT 2100
Db 2041 AAGTCATGGTTGACGAATGCTAACTTTAGACCACGAGGTTGGAGTCCCTCAACGATTTT 2100
Qy 2101 CCATAAGGCTTGGTGGATAGTGTGATTAACAAGCAAAATGGCATCGGTGTCTACACTGG 2160
Db 2101 CCATAAGGCTTGGTGGATAGTGTGATTAACAAGCAAAATGGCATCGGTGTCTACACTGG 2160
Qy 2161 CTCACTCAAAAGTTCAAACAAATGAAGAACTATGTGGACAGTTTGGCAGCTTCGTTGTCGCG 2220
Db 2161 CTCACTCAAAAGTTCAAACAAATGAAGAACTATGTGGACAGTTTGGCAGCTTCGTTGTCGCG 2220

Db 4381 GAAAGCGGTGATGTGACTACTTTTCATCGGCAATPACTGTTATATAATAGCAGCTTGCCTTGGG 4440
Qy 4441 TTCAATGTTACCGATGGAAAGGTCATAAAAGTGCTTTTGTGTGGAGACGATTCGGTTTTT 4500
Db 4441 TTCAATGTTACCGATGGAAAGGTCATAAAAGTGCTTTTGTGTGGAGACGATTCGGTTTTT 4500
Qy 4501 GTATTTTCCAAAGGGTTTGGATTTCCCTGACATTCAGTCATGCTCAATCTCATGTGGAA 4560
Db 4501 GTATTTTCCAAAGGGTTTGGATTTCCCTGACATTCAGTCATGCTCAATCTCATGTGGAA 4560
Qy 4561 TTTTGGAGCCAAACCTGTATAGAAAGAGTACGGTTACTTTTTGGTGTAGATACATCATACA 4620
Db 4561 TTTTGGAGCCAAACCTGTATAGAAAGAGTACGGTTACTTTTTGGTGTAGATACATCATACA 4620
Qy 4621 CCATGATAAGGGAGCAATAGTGTATATGATTCCTTTGAAGTTGATCTCCAACTTGGGGC 4680
Db 4621 CCATGATAAGGGAGCAATAGTGTATATGATTCCTTTGAAGTTGATCTCCAACTTGGGGC 4680
Qy 4681 AAAACATATCAAGGATTTATGATCACTTAGAAGAGTTAAGGGTGTCTTTGTGCGATGTTC 4740
Db 4681 AAAACATATCAAGGATTTATGATCACTTAGAAGAGTTAAGGGTGTCTTTGTGCGATGTTC 4740
Qy 4741 TTGTTCCGCTCGAAACTGGTCTTTAGGCTTTCCGAGCTGAACGAGCTATCAAGGAGGT 4800
Db 4741 TTGTTCCGCTCGAAACTGGTCTTTAGGCTTTCCGAGCTGAACGAGCTATCAAGGAGGT 4800
Qy 4801 TCATAAAACCGCGATTTGATGGTTCGTTTGTCTTTTAAATTTGTTTAAACAAATTTTGTGTGA 4860
Db 4801 TCATAAAACCGCGATTTGATGGTTCGTTTGTCTTTTAAATTTGTTTAAACAAATTTTGTGTGA 4860
Qy 4861 TAAATTTTATTTAGAACTTTGTTTAAATTTGCTTTAGTCTCAGAGATCTGTCAAAA 4920
Db 4861 TAAATTTTATTTAGAACTTTGTTTAAATTTGCTTTAGTCTCAGAGATCTGTCAAAA 4920
Qy 4921 TTACGGAGTTCATTTGATCTTTTAAACAGGATGAGATCTTTCCGGCATTTCAATGACTAAGG 4980
Db 4921 TTACGGAGTTCATTTGATCTTTTAAACAGGATGAGATCTTTCCGGCATTTCAATGACTAAGG 4980
Qy 4981 TCAAGAGTGTAGAAATATCGACTGTGGACAGATTTATGGCTGTTAAGAAATGATAGTCTTT 5040
Db 4981 TCAAGAGTGTAGAAATATCGACTGTGGACAGATTTATGGCTGTTAAGAAATGATAGTCTTT 5040
Qy 5041 CTGATGTAGATTTACTTTAAAGGTGTTAAGTTAGTTAAGAAAGGATGTGTGCTTAGCTG 5100
Db 5041 CTGATGTAGATTTACTTTAAAGGTGTTAAGTTAGTTAAGAAAGGATGTGTGCTTAGCTG 5100
Qy 5101 ATTTGGTAGTCTCTGGGAGTGGAATCTCCGGGATACTGCGGTGCTGCTCAGTGTGTT 5160
Db 5101 ATTTGGTAGTCTCTGGGAGTGGAATCTCCGGGATACTGCGGTGCTGCTCAGTGTGTT 5160
Qy 5161 GTATTTGTAGATAAGAAATGAAAAGGAGTAAAGGAAGCAACGCTGGGTGCGTATCACGCC 5220
Db 5161 GTATTTGTAGATAAGAAATGAAAAGGAGTAAAGGAAGCAACGCTGGGTGCGTATCACGCC 5220
Qy 5221 CTGCTTGCAAAAAGAAATTTTCTTTTAAAGCTAATCCCTAATTTCAATAACATCCGAGG 5280
Db 5221 CTGCTTGCAAAAAGAAATTTTCTTTTAAAGCTAATCCCTAATTTCAATAACATCCGAGG 5280
Qy 5281 ATGCTGAGAGCAACCGTGGAAGTGTGTAGTGAATATCAAAAGGAGTGGCTATGGAAGAAG 5340
Db 5281 ATGCTGAGAGCAACCGTGGAAGTGTGTAGTGAATATCAAAAGGAGTGGCTATGGAAGAAG 5340
Qy 5341 GATAGTCTCTTTTATCTTTGGAGTTCGTTTCAATTTGTGTAGTACATAAAAATTAATGTAA 5400
Db 5341 GATAGTCTCTTTTATCTTTGGAGTTCGTTTCAATTTGTGTAGTACATAAAAATTAATGTAA 5400
Qy 5401 GAAAAGTTTGGAGGAAGCTATTTTGTAGTGTGACAGAGGCTCCGCAATTCGACTCACTG 5460
Db 5401 GAAAAGTTTGGAGGAAGCTATTTTGTAGTGTGACAGAGGCTCCGCAATTCGACTCACTG 5460
Qy 5461 AAAAGGTTTGGAGGAGTTCGTGGATGAAGTACCAATGGCTGTGAAACTCGAAAAGGTTTC 5520
Db 5461 AAAAGGTTTGGAGGAGTTCGTGGATGAAGTACCAATGGCTGTGAAACTCGAAAAGGTTTC 5520

Qy 5521 CGGAAAAAAGAAATGGTAGGTAATTAATGTTTAATAAAGAAAAATAAATAACAGTG 5580
Db 5521 CGGAAAAAAGAAATGGTAGGTAATTAATGTTTAATAAAGAAAAATAAATAACAGTG 5580
Qy 5581 GTAAGAAGGGTTTTAAAAATTGAGGAATTCAGGATTAATGTAAGTGAACGAGTCTATCG 5640
Db 5581 GTAAGAAGGGTTTTAAAAATTGAGGAATTCAGGATTAATGTAAGTGAACGAGTCTATCG 5640
Qy 5641 CGTCATCGAGTACGTTTTTAATCAATATGCTCTTATACAACTCAACTCTCCGAGCCAAATTTGT 5700
Db 5641 CGTCATCGAGTACGTTTTTAATCAATATGCTCTTATACAACTCAACTCTCCGAGCCAAATTTGT 5700
Qy 5701 TTACTTATCTTCCGCTTACCGAGATCTGTGAGCTGATCAATCTGTGTCAAAATGCATT 5760
Db 5701 TTACTTATCTTCCGCTTACCGAGATCTGTGAGCTGATCAATCTGTGTCAAAATGCATT 5760
Qy 5761 GGGTAACCACTTTTCAACGCAACAAAGCTAGGACAAAGTCCACAGCAATTTGCGGATGC 5820
Db 5761 GGGTAACCACTTTTCAACGCAACAAAGCTAGGACAAAGTCCACAGCAATTTGCGGATGC 5820
Qy 5821 CTGGAACCTGTGCTAGTATGACAGTGAGATTTCTGTCATCGGATTTCTATGTGTATAG 5880
Db 5821 CTGGAACCTGTGCTAGTATGACAGTGAGATTTCTGTCATCGGATTTCTATGTGTATAG 5880
Qy 5881 ATATAATTCGACGCTTGATCCGTTGATCACGGGTTTAAATAAGCTTTGATACAGAAA 5940
Db 5881 ATATAATTCGACGCTTGATCCGTTGATCACGGGTTTAAATAAGCTTTGATACAGAAA 5940
Qy 5941 TAGAATAATAGAGTTGATTAATCAACCCGACCGAATCTACTCAAAATCGTTAAACGGAC 6000
Db 5941 TAGAATAATAGAGTTGATTAATCAACCCGACCGAATCTACTCAAAATCGTTAAACGGAC 6000
Qy 6001 TCAGAGGTAGACGATCTACTGTAGCTATAAGGGCTTCAATCAATAATTTGGCTAATGA 6060
Db 6001 TCAGAGGTAGACGATCTACTGTAGCTATAAGGGCTTCAATCAATAATTTGGCTAATGA 6060
Qy 6061 ACTGGTTCTGGAACTGGCATGTTCAATCAAGCAGGCTTTGAGACTGCTAGTGGACTTGT 6120
Db 6061 ACTGGTTCTGGAACTGGCATGTTCAATCAAGCAGGCTTTGAGACTGCTAGTGGACTTGT 6120
Qy 6121 CTGGACCAACACTCCGGTACTTAGCTATTTGTTGTGAGATTTCTTAAATAAAGTCCGCTG 6180
Db 6121 CTGGACCAACACTCCGGTACTTAGCTATTTGTTGTGAGATTTCTTAAATAAAGTCCGCTG 6180
Qy 6181 AAGACTTAAATTCAGGGTGGCTGATACCAAAATCAGCAGTGGTTGTTCTGCCACTTAAA 6240
Db 6181 AAGACTTAAATTCAGGGTGGCTGATACCAAAATCAGCAGTGGTTGTTCTGCCACTTAAA 6240
Qy 6241 TATAACGATTTGATCTGGATCCAAACAGTTAAACCATGTGATGGTGTATCTGTGGTA 6300
Db 6241 TATAACGATTTGATCTGGATCCAAACAGTTAAACCATGTGATGGTGTATCTGTGGTA 6300
Qy 6301 TGGGTAACCAATCGGAGAGGTTTCAATCTCCCTAACCCGCGGTAGCGGCCA 6355
Db 6301 TGGGTAACCAATCGGAGAGGTTTCAATCTCCCTAACCCGCGGTAGCGGCCA 6355

RESULT 2
US-09-962-527-1
; Sequence 1, Application US/09962527
; Publication No. US20030049813A1
; GENERAL INFORMATION:
; APPLICANT: GARGER, STEPHEN
; HOLTZ, R. BARRY
; MCCULLOCH, MICHAEL
; TURNER, THOMAS
; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
; PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
; FROM PLANT SOURCES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon

QY 1640 TATGTCATGGAAGACAGGCTTCGTAGCTGAATACACCAAGTCTGAGGAGTTACCCGAT 1699
D 1638 UAUGGACCUUCCACGACGAUUAUGACGAGUACAGGCGCUCUGUGGACGAUGCCUGCG 1697
QY 1700 CTAGATATCAAGAGGACTTAGAAGAGCTGAGCAATATGACGCGGTTATCAGATTA 1759
D 1698 CUUGACAUUAGGAAGAAGUAGGAAGAACGGAAGUGAUGACAAUGCACUUUCAGAGUUA 1757
QY 1760 TCTATCCTTAAGGCTGCTGATAATTTGCGATATCGGAAGTTTCAAAGACATGTGCAAGGCT 1819
D 1758 UCGGUGUAAGGAGUCUGACAAAUUCGAUUGAUGUUUUCGAGUGGCCAUAUCU 1817
QY 1820 TTAGATGTTAGTCTGTGATGCGACGACGAGTAATCGTTGAGGCGCGGAATAGAAAGC 1879
D 1818 UUGGAAGTUGACCCAAUGACGCGACGAGGAAUUAUAGTUCGCGUACGAGCAUAGAGAGC 1877
QY 1880 GGTTTAACTCTTACTTTTGTATAGCCAAACGAGGAGATGTGGCTAAGGCTCT-----T 1933
D 1878 GGUCUGACUCUCACAUUUGAACGACCUACUGAGGCGAAUUGUGCGUAGCUUUAACGAGU 1937
QY 1934 AAAAGCAGCGGCTCTGAGGCGGTGTATGTCTTGAACCGACATCCGAAGAGGTGAACGTA 1993
D 1938 CAAGAGAGGCUUCAGAGGUGCAUUGUAUUAUCUACAGAGAAUGUAAGAACCGUCC 1997
QY 1994 AATAAATTTTCTATTGCTGAGAAAGGAGATGTGCTGTGTGTCAGAAAGTCATGTTTG 2053
D 1998 AUGAAGGUGUCGAGGCGCAGAGGAGAGUUAUUAUUGUGGUGUUGGAGUACUCCG 2057
QY 2054 ACGNATGCTAACTTAGAGCACCAGGAGTTGAGTCCCTCAACGATTTCCATAAGGCTTGC 2113
D 2058 GAGUCGUCUAUUCUUAAGAACGAGAGAUAGAGUCUUUAGAGCAGUUAUUAUUGGCGACG 2117
QY 2114 GTGGATAGTGTGATTAACAAGCAATGCGATCGGTTGTCTACACTGGCTCACTCAAAAGTT 2173
D 2118 GCAGUUGUUAUUCUAGACAGAGUCUCGAGUUGUUAUACGCGGUCGGAUUAAGUU 2177
QY 2174 CAACAATGAGAACTATGTGACAGTTGGCAGCTTGGTGTGCGGCACATGTATCAAT 2233
D 2178 CAGAAAUGAAAAUUCUUAUUGCUGGAGCAUUAUUGGUGGUGGUGGUGGUGGUGGUGG 2237
QY 2234 CTATGCAAGTCACTAAAGGATGAGTGGGTATGATTTCTGATTTCCAGGAGAAAGTTGGT 2293
D 2238 CUCGUCAGAAUCCUUAAGAUACAGCUGCUUAUUGAACCUUGAAACCCGUCUAAAGUUUGGA 2297
QY 2294 GTTTGGGATGCTTTGAAAAAGTGGCTCTCAAACTGCGGCGCAAAAGGTCATTCATGG 2353
D 2298 GUCUGAUGUUGCAUUGAAGUGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2357
QY 2354 GGAGTTGCTGGGATTAAGGGGAAATGTTTACTGCACTTCTATCTTATGAAGAGAT 2413
D 2358 GGUGUGUGAAAAACCCACGAGGAAAGUUAUUGUGGCGCUUUGGAAUUAUGAUGACG 2417
QY 2414 AGAATGTTGACTGAGGCTGAGGAGGTTGCTGTATCATCTGATACATGATATAT 2473
D 2418 GGUGUGUGCAUUGCUGAUGAUGAGAGAGUAGUCUGUUAUUGCUGAGUCUGUUGUUUAU 2477
QY 2474 TCTGATATTGCAAAAGTCCAAATCTGAGGAAAAAACAATGAGAGACGCTGAACCCCAAGAA 2533
D 2478 UCCGACAUUGGCAAAUUCAGAAUUCUGCGCAGACUGCUUGCAACGAGAAACCGCAUGUC 2537
QY 2534 CCTACTGAAAGATGGTACTTGTGATGGGTGCTGCTGTGTGGAAGATCAAAAGGAGAT 2593
D 2538 AGUAGCGCAAAAGGUGUUGUUGGACGAGUUCGCGGCGUGGAAAAAACAAGAAAAU 2597
QY 2594 TTTGAAAGATTTGATCTTGATGAGATTTGATCTTGGTTCTGAAAAACAGCTGCTGCT 2653
D 2598 CUUCCACGGGUUAUUAUUGAUGAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2657
QY 2654 ATGATCAGAAAGAGGGTAAATTTCACTGTGATGAAGAGCCCAATGGAACAATGTGAGA 2713
D 2658 AUGAUCAGAGACGCGGCAUUCUUCAGGGAUUAUUGGCGCACGAGGACCAACGUAUAA 2717

QY 2714 ACGGTAGATTCACTTCTAATGCTAT-----CCAAAACCGCGATCACACAGAGGCTT 2764
D 2718 ACCUGUAUUCUUCUUGAUGAUAUUUGGAAAAAGCACACGCGUGUCAGUUUCAAAGAGUUA 2777
QY 2765 TTTATTGATGAAGGGTGTGTCACACCGGTTGTGTAACTTCTCTGGTGTCTTATCTCT 2824
D 2778 UUCAUUGAUGAAGGGUUGAUGUUGCAUUGGUGUUAUUUUCUUGGCGGAGUCA 2837
QY 2825 GGTTCGACATCCCATACATTTTACGAGATACACAGCAGATTTCTTTTATTAACAGATT 2884
D 2838 UUGGCGCAAUUUGCAUUGUUUACGGAGACACACAGCAGAUUCCAUAUUAUAGAGU 2897
QY 2885 CAGAAATTTCCGCTATCCCAACATTTTGAGAACTGCAAGTGGATGAGTGGAGG 2944
D 2898 UCAGGAUUCGCGACCCGCAUUAUUGCCAAUUGGAUUGACGAGGUGGAGACAGC 2957
QY 2945 AGGACACACTGAGATGCCCGAGTGATGCAATTTTCTCAATCGAATCGAAAGGA 3004
D 2958 AGAACUACUCUCGUGUUGCCGCGAGUCACAUUUCUGAACAGGAGUAUUGAGGCG 3017
QY 3005 GCGGTGACAAACCACTTCAACTGTACAAAGATCGGTCATCTGAGATGATAGGCGGTAAG 3064
D 3018 UUGUCAUGACACUUCUUGUUUAAAAGUCUGUUGCGCAGGAGUUGGCGCGAGCC 3077
QY 3065 GGAGTACTAAAGTGTTCCTCAACCACTAAAAGGNAATTTGTAATTTTCACTCAGGCT 3124
D 3078 GCGUGAUAUUCGAGUCUCAAACCCUUGCAUGGCAAGAUCCUGACUUUUAUCCCAUUG 3137
QY 3125 GATTAATTTTTCAGTTAGAGGAGAGGCTATAAGATGTGAACACCGTTTCATGAGATCCAA 3184
D 3138 GAUAAAGACUCUCUGUUUUAAGAGGUAUUAUAGUUUUCACUCUGUGCAUGAUGUCAA 3197
QY 3185 GAGAAACCTTTGAAGATGTGCTGTCGTCAGATTGACGCAACTCCACTGACTCTGATT 3244
D 3198 GCGAGAGACUACUCUGAUGUUUCACUAGUUAAGUUAACCCUACACACGAGUCCUCAU 3257
QY 3245 TCCAGTCTTCCCGCATGTTCTAGTCGCTCTGACTAGACACACAAAGAGGTTCAATAT 3304
D 3258 GCAGGAGACAGCCCAUGUUUGGCGCAUUGCAAGGACACACCCUGUUGCUCUAAUAC 3317
QY 3305 TACACCTAGTGTAGATCTTTAGTACAGATAATTTAGTGTGTTGTTCTTTTAAGTCC 3364
D 3318 UACACUGUUAUGAUGAUCCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3377
QY 3365 TTTCTTTTGAATAATGTTAGTGAAGCAGGAGTGTAGTAGCAATTAAGATGATGCA 3424
D 3378 UACUUGUUAUUAUUAAGGUGCUGAUGAGGAAACACAAUAGCAAUUACAGAUUAGUC 3437
QY 3425 GTGTTCAAGGTATATCTCTTTGTCGCAACCTTAATTCAGGAGACTTTCCAGATCTA 3484
D 3438 GUGUCAAAGGUCCAAUUCUUUUGGAGCGCCAAAGACUGGUGAUAUUAUUGAUAUG 3497
QY 3485 CAGTTCTATTACGATGATGCTCCCTGTTGTAATAGTACTATCTTAACAAGTATGATGCT 3544
D 3498 CAGUUUAUUAUUAUUAUGUUCUCCAGGCAACAGCACCAUGAUGAUAUUAUUAUGUC 3557
QY 3545 GTTACCATGAGGTTACGTCGATAATAGTCTTTAATGTGAAGGATGTGTCTTGTATTTCC 3604
D 3558 GUUACCAUGAGGUGAUGACAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3617
QY 3605 AAAAGTATTCGATGCCAAAGGAGGTGAACCATGTCTAGAGCCAGTTTTCGCTACCGCG 3664
D 3618 AAGUCUGUUGCGCGCUAAGGAUCAAUCAAACCAUUAUUAUUAUUAUUAUUAUUAUUAU 3677
QY 3665 GCGGAACCGCAAGGGCTGAGGACTACTCGAAATCTGTTGTAATGATTTAAAGAAAT 3724
D 3678 GCAGAAUAGCCACGCCAGACUGGACUUAUUGAUAUUAUUAUUAUUAUUAUUAUUAU 3737
QY 3725 TTCAACGCACAGACCTGACGCGGACGATTAATGACATTCAGAGACCGCATCTGTTGTAGA 3784
D 3738 UUAACGCACCGAGUUGUGGCAUCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3797
QY 3785 GATAAGTTTTTGTAGTACCTATTTTATTAATAAAGAAAAATACACAAAAAATATTGCTGGA 3844

Db 3078 GCCGUGAUCAAUCCGAUCUCAAACCCUUGCAUGGCAAGAUCCUGACUUUUAACCAUUCG 3137
Qy 3125 GATAAATTTGATTAGAGAGAAAGGGCTATTAAGAAATGTGAACACCGTTTCATGAGATCCAA 3184
Db 3138 GAUAAAGAGCUCUGCUUUUCAAAGAGGUUAUCAGAGUUAUCACUGUGCAUGAAGUGCAA 3197
Qy 3185 GGAGAAACCTTTGAAGATGTCTCGTGTAGATTGAGTGAAGCAATCCACTGACTCTGATT 3244
Db 3198 GGCAGACAUAUCUGAUGUUUACUAUUAAGGUUAACCCUACACCAUGCUUUAUGCAU 3257
Qy 3245 TCCAAAGTCTTCCCGCATGTTCTAGTCGCTCTGACTAGACACACAAGAGAGCTTCAAAATAT 3304
Db 3258 GCAGAGACGCCACAUUUUUGUGCGAUUGUCNAGGACACACUGUUCGCUCAAGUAC 3317
Qy 3305 TACACCGTAGTGTAGATCCCTTTTAGTACAGATAATAGTAGTGTCTTCTTTTAAGCTCC 3364
Db 3318 UACACUGUUAUGGAUCCUUUAGUUAUUAUAGAUCAUUAAGAGAUCAUGAGAAACUUAUGCUG 3377
Qy 3365 TTCCTTTTAGAAATGTATATGTTAGAACGAGGTAGTAGCAATTCACAGATGATGCA 3424
Db 3378 UACUUGUUAUUAUGUAUUAAGUGCAUGCAAGGAACACAUAUAGCAUAUACAGAUUGACUG 3437
Qy 3425 GTGTTCAAGGTCAATCTCTTTGTGGCAACACCTAAATCAGGAGACTTTCCAGATCTA 3484
Db 3438 GUGUCAAAGGUUCCAUUUUUUGUCAGCGGCCAAAGACUGUGUAUUUUUGUAUUG 3497
Qy 3485 CAGTCTATTACGATGTATGCTCCCTGGTAAATAGTACTATCTTAACAAAGTATGATGCT 3544
Db 3498 CAGUUUAUUAUGUAUUAAGUGUCGCCAGGCAACAGCACCAUGAUAUUAUUGAUGCU 3557
Qy 3545 GTTACCATGAGGTACGTGATAATAGTCTTAATGTGAAGGATTGTCTTCTGATTTTCC 3604
Db 3558 GUUACCAUGAGGUGAUCGACUAUUAUGAAUGUCAAGAAUGCAUAUUGGAUUGUCU 3617
Qy 3605 AAAAGTATTCGATGCCAAAGAGGTGAACCATGTCTAGAGCCAGTTTTCGCTACCGCG 3664
Db 3618 AAGUCUUGUUGCGCUUAAGGAUCAAUAACAAACCAUAUAUCCUUAUGUAACGACGCG 3677
Qy 3665 CGGAACCGCCAAAGGGTGCAGGACTACTCGAAATCTGGTTGCAATGATTAAAGAAAT 3724
Db 3678 GCAGAAUUGCCACGCGACUGGACUAUUGGAAAUUAUUGGCGCAUGAUUAAAGAAAC 3737
Qy 3725 TTCACGCCACGACCTGACCGGGACGATTGACATTGAGACACCGCATCTGTTGTAGTA 3784
Db 3738 UUAACCGCACCGGACUGUGUCUGGCAUCAUUAUGAUUUGAAAUUAUCUGCAUCUUUGUGUA 3797
Qy 3785 GATAAGTTTTTGTAGTATTTTATTAAAAAGAAATAACAAAAATATTGCTGGA 3844
Db 3798 GAUAAUUUUUUGUAUUAUUGCUUAAGAAAGAAAGAAACCAAAUAAAUUAUUGUUCU 3857
Qy 3845 GTGATGACGAAGGATTCATGATGAGATGGTTGGAAACACAGAAAGAGTACTATTGGAC 3904
Db 3858 UUGUUCAGUAGAGAGUCUCUCAAUAGAUUGGUUAGAAAGCAGGAACAGGUAACAAUAGGC 3917
Qy 3905 GACTTGGCTACTACAAATTTTACAGATCTCGGGCCATCGATGATCAAGACACATGATC 3964
Db 3918 CAGUCGCAUUAUUGAUUUGGUAUUUGCGCAGCAUGUUCAGUACAGACACACAGAUU 3977
Qy 3965 AAGGCTCAACCAACAGAAATTGGACCTTTCAATTCAAGATGAATACCTGCTCTGCAA 4024
Db 3978 AAAGCAAAACCAAAAGUUGGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4037
Qy 4025 ACAATTGCTACCAATTCGAAGCAGATCAACGGTATTTTGGCGGTTTCTCA---GAGCTT 4081
Db 4038 ACGAUGUGUACCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4097
Qy 4082 ACAGAGTTGCTGCTCGAGCATTTGATTTCTAAGAGTTTCTTTCTTTTACTAGGAACCT 4141
Db 4098 ACUAGGCAAUUAUCUGGACAGUUGUUAUUCGAGCAGAUUUUUUUUUUUUUUUUUUUUUUU 4157
Qy 4142 CCAGAAACAGATTCAGAAATTTTCTCGGATCTCGACTCGACGCTGCTTCTTATCGATGTGTTA 4201
Db 4158 CCAGCGCAGAUUUGAGGAUUUUCUGGAGAUUCUCGACAGUUGCGCGGUAUGGUAUGUCUUG 4217

Qy 4202 GAACGTGATATTTCTTAAGTATGATAGTCAAGAACAGATTTTCATTGCTGTGTAGATAT 4261
Db 4218 GAGCUGGAUUAUCAAUAUACGACAAAUUCUCAGAAUUAUUAUUAUUAUUAUUAUUAUUA 4277
Qy 4262 GAAATATGGAAGAAAGATTGGGTCTCAATGAGTTTTTGGCCGAGATGTGGAACAAGGGCAC 4321
Db 4278 GAGAUUGGCGAUAUUGGUUUUUAAGACAUUUUGGGAGAAUUUUGGAAACAAGGGCAU 4337
Qy 4322 AGGAAACAATCTTTGAAGGATTAATCTGCTGGAATCAAGACATGCTGTGTGTATCAAAAG 4381
Db 4338 AGAAAGACCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4397
Qy 4382 AAAAGCGGTGATGTGACTATTTTCATCGGCATCTGTTTATAATAGCAGCTTGTGTGGGT 4441
Db 4398 AAGAGCGGGACGUCACGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4457
Qy 4442 TCAATGTTACCGATGGGAAAGGTCTATATAAGGTCTTTTGTGTGAGACGATTCGTTTGTG 4501
Db 4458 UCGAUGCUUCGGAUGGAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4517
Qy 4502 TATTTTCAAAGGGTTTTGGATTTCCCTGACATTCAGTCTGCTGCTTAATCTCATGTGGAAT 4561
Db 4518 UACUUUCCAAAGGGUUGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4577
Qy 4562 TTTGAGGCCAAAATGTATAGAAAGAGTACGTTTACTTTTGTGTGTAGATATCATATCAC 4621
Db 4578 UUGAAGCAAAAACUGUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4637
Qy 4622 CATGATAGGAGCAATAGTGTATTATGATCTTTTGAAGTTGATCTCAAACTTTGGGCA 4681
Db 4638 CACACAGAGAUUGCAUUGUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4697
Qy 4682 AAAATATCAAGGATTTATGATCACTTAGAAGAGTTAAGGGTGTCTTTTGTGCGATGTTGCT 4741
Db 4698 AAACACAUAAGGAUUGGAAACACUUGAGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUA 4757
Qy 4742 TGTTCGCTCGAAACTCGTGTGCTTAGGCTTTCCGAGCTGAACGACGATATCAAGAGGTT 4801
Db 4758 GUUUCGUU---GAACAAUUGUGCGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4814
Qy 4802 CATAAAACCGGATTTGATGTTGCTTTGCTTTTAAATGTTGTTAAACAAATTTTGTGTGAT 4861
Db 4815 CAUAAAGACCGCCUCCAGGUUUGUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4874
Qy 4862 AAATTTTTATTAGAACCTTTGTTTTTAAATGGCTGTAGTCTCAGAGATCTGTCAAAAT 4921
Db 4875 AAAGUUCUUUAAGAUUGUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4934
Qy 4922 TAGCGAGTTCAATGATCTTTTCGAAAACAGGATGAGATACTTCCGCGATTCATGACTAGGT 4981
Db 4935 CAUAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4994
Qy 4982 CAAGAGTTTAGAATATCGACTGTGGACAAGATATGCTGTGTTAAGAAATGATGCTTTTC 5041
Db 4995 AAAGAGUUUAUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5054
Qy 5042 TGATGTAGATTTACTTAAAGGTGTTAAGTTAGTTAAGAAAGGGTATGTGTGCTTGTAGCTGA 5101
Db 5055 AGAGGUAACCUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5114
Qy 5102 TTTGCTAGTGTCTGGGAGTGAATCTCCCGATACTGCGGTGTGTGTGTGTGTGTGTGTGTGT 5161
Db 5115 UUGUGUCGUCACGGCGAGUGGAAACUUGCCUGACAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5174
Qy 5162 TATTGTAGATAAGAGATGAAGAGGAGTAAAGAGCAACGCTGGGTGCTGATCAACGCCCC 5221
Db 5175 UCUGUGGACAAAGAGGAGGAAAGAGCGGACGAGGCCACUUCUGGAUUAUUAUUAUUAUUA 5234
Qy 5222 TGCTTGCAAAAGAAATTTTCTTTTAAAGTAAATCCCTTAATTTTCAATTAATTCGAGGA 5281
Db 5235 AGCUGCAAAAGAAAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5294


```
QY 5282 TGCTGAGAGACCCGTCGCAAGTGTGTAGTGAATATCAAGAGGTGGCTATGGAAGAAG 5341
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5295 CGCGAUGAAAACGUCUGCGCAAGUUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUA 5354
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5342 ATACTGTCCTTTATTTTGGAGTTCGTTTCAATTTGTGTAGTACATATAAATATGTAAG 5401
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5355 UUCUCUGCGUUCUCUGCGAGUUGUGUGUGUGUUAUAUAUAUAUAUAUAUAUAUAUA 5414
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5402 AAAAGTTTGGAGGACGATTTTTCAGTGTGACACGCGCTCGCCAAATGGAATCACTGA 5461
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5415 AUUAGUUUAGAGAGAAGAUUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUA 5474
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5462 AAAAGTTTGGAGGAGTTTCTGTGATGAAGTACCAATGCTGTGAATTCGAAAAGTTTC- 5520
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5475 AGAAGUCUGAUGAUGUUAUGAAGAUUGUCCUAUGUGAUGCAUGGCUUGCAAGUUUCG 5534
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5521 -----CGGAAAACAAAAGAAATGTTAGTGTATATATATATATATATATAT- 5561
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5535 AUCUCGAACCGGAAAAAGAGUGUGUGCGCAAGGGGAAAAUAUGAUAUGAUCGGUC 5594
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5562 -----AAGAAATAAATAACAGTGTAAAGAGGTTTAAATTTGAGGAATTTGAGA 5614
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5595 AGUGCCGACAGAAACUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUA 5654
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5615 TAATGTAAGTGTATGACGAGT-----CTATCGCGTCATCGAGTACGTTTATCAAT 5665
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5655 UAAUUUAUCGAUGAUGAUGUCCGAGGCUACUGCGCAAGCGGAUUGUUUA---AAU 5711
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5666 ATGCTTTATACAACTCTCCGAGCCAAATTTGTTTACTTATCTTCGCTTACCAGAT 5725
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5712 AUGUCUUAAGUAUCACUACUACUACUACUACUACUACUACUACUACUACUACUAC 5771
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5786 GCTAGCAACAAGTCAACAGCAATTTGCGGATGCTGTGAAACCTGTGCTAGTAGACA 5845
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5832 GCUCGAAACUGUGUUCNAAGACAUAUCAGUGAGUGUGGAAACCUACCAAGUAACU 5891
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5846 GTGAGATTTCTGCAATCGGATTTCTATGTGTATAGATATAATTCAGCGCTTGATCGTTG 5905
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5892 GUUAGGUUCCUGACAGUACUUAUAAGUGUACAGUAUAUAUGCGGUUAUAUAGACCGCUA 5951
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5906 ATCAAGCGCTTATTAATAGCTTTGATCTAGAAATAGAAATATAGAGGTTTCAATCAA 5965
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5952 GUCACAGCACUGUUAAGGUGCAUUCGACACUAGAUAUAUAUAUAUAUAUAUAUAUA 6011
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5966 CCGCACCGAATACTACTGAAATCGTTAAACGCGACTCAGAGGCTAGACGATCTACTGTA 6025
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 6012 GCGAACCCACGACUGCCGAGAGUUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUA 6071
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 6026 GCTATAAGGGCTTCAATCAATTAATTTGGTGAATGAATCTGGTTCGTGGAATCTGGCATGTT 6085
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 6072 GCAUAAGGAGCGCAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUA 6131
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 6086 AATCAAGCAGGCTTTGAGACTGCTAGTGTGCTGAGCACTGCTGAGCACTCGGCTACTTAG 6145
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 6132 AAUCGGAGCUCUUCUGAGAGCUCUUCUGUUGUUGUUGACCUUGGCUUGCAACU--- 6188
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 6146 CTATTGCTGTGAGATTTCTAAATAAAGTCGCTGAAGACTTTAAATTCAGGCTGCTGCA 6205
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 6189 -UGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 6246
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 6206 TACCAAAATCAGCAGTGGTGTGTCGTCCTTAATTAATTAATTAATTAATTAATTAATTA 6265
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 6247 UACGAUAACGAUAGUUGUUUUCUCCACUUAUAUAUAUAUAUAUAUAUAUAUAUAUA 6305
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 6266 AACAGTTAAACCAATGTGTGTATATCTGTGTATGCGGTAAACATCGGAGGTTTCG 6325
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 6306 GCGGGUCAAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUA 6365
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 6326 AATCCTCCCTAACCGCGGTAGCGGCCCA 6355
```

```
Db 6366 AAUCCCCCGUUAUACCCCGGUAGGGGCCCA 6395
```

RESULT 4

```
US-10-338-592-2
; Sequence 2, Application US/10338592
; Publication No. US20030208792A1
; GENERAL INFORMATION:
; APPLICANT: Pitchen, John H.
; APPLICANT: Beachy, Roger N.
; TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS TO
; PRODUCE PEPTIDES AND PROTEINS
; FILE OF INVENTION: OVERPRODUCE PEPTIDES AND PROTEINS
; FILE REFERENCE: TSRI 312.1C1
; CURRENT APPLICATION NUMBER: US/10/338,592
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 09/401,415
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 08/687,559
; PRIOR FILING DATE: 1996-11-18
; PRIOR APPLICATION NUMBER: PCT/US95/01467
; PRIOR FILING DATE: 1995-02-03
; PRIOR APPLICATION NUMBER: US 08/192,477
; PRIOR FILING DATE: 1994-02-03
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 6395
; TYPE: DNA
; ORGANISM: Tobacco mosaic virus
US-10-338-592-2
```

Query Match 38.8%; Score 2466.4; DB 17; Length 6395;

Best Local Similarity 63.0%; Pred. No. 0;

Matches 4023; Conservative 0; Mismatches 2301; Indels 66; Gaps 11;

```
QY 20 ACAACAATTAATAAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 79
Db 18 ACCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 77
QY 80 ATACAACTTAATAATTAAGCAACGCCCTTCTTGAACCGTGTAGTGTAAACAACAACA 139
Db 78 ACACAGACAGTACCAATTCAGCTTTGCTGGACACTGTCCGAGGAAACAACAACAACA 137
QY 140 AATGACCTTTCGAAGAAGCGCATGTACGATACGCGCGTGTGGAAGAAATTAACGCCG 199
Db 138 AATGATCTAGCAACGCTGCTTTACGACACAGCGTGTGAAGAGTTTAAACGCTGTG 197
QY 200 CGTAGACCAAAAGGTCAACTTTTCCAAAATAATAGGGAAGCAAAACGCTTCTAGTCTCC 259
Db 198 CGAGGCGCAAGGTGAACCTTTTCAAAAGTAATAAGCGAGGAGCAGACGCTTATTGCTAC 257
QY 260 AACGCGTACCGGAGTTCAGATTACCTTTTATATATCTCAAAATGCGGTACACAGTTTG 319
Db 258 CGGCGGTATCCAGAAATTCAAATTTACATTTTATAACACGCAAAATGCGGTGATTCG 317
QY 320 GCTGAGGTTTTCAGAGCAATTAAGAAATCTGATCTACAAGTTCCCTATGATCG 379
Db 318 GCAGGTGATTCGATCTTTAGAACTGGAATATCTGATGATCAAAATTCCTTACGATCA 377
QY 380 CCGACATATGATATAGTGGGAACTTTTCAGACACATTTTTCAGAGGAGGATACGTT 439
Db 378 TTGACTTATGACATAGGCGGAAATTTTGCATCGCATCTGTTCAAGGAGGAGCAGCATAT 437
QY 440 CATTCCTGTATCCCAATCTGACATAGAGATATAATAGGACGACGAGCAAGCAAAAGGAC 499
Db 438 CACTGCTGATCCCAACCTGCGATCTCGGACATCATCGGACACGAGCCAGCAAGAAC 497
QY 500 TCAATTGAGATGATTTTGTCCAGATTGCTCCGTTCTTAAACAAGGTAATTCCTGAGTTCAA 559
Db 498 AGTATTGAATATATCTTTCTAGGCTAGAGAGGGGGGAAACAACAGTCCCAACTTCCAA 557
QY 560 AGGAGGCTTTTAAACAGGTATGACAGAGCTCCCAACGAAGTCTGCTGCTCTAAACCTTTT 619
```

Db 558 AAGNAGCAATTTGACAGATACGCAAAATTTCTGAGACGCTGCTGTCACAAATCTTTC 617
Qy 620 CAGGATTGTGCAATACATPCGCCCGCAGAGAAATAGTGGTAGAAGATACGCTGTTGCTCTGCAC 679
Db 618 CAGCAATGCGACATCAGCCGATGCGCAATCAGCAGAGTGATGCCATTGCGCTACAC 677
Qy 680 AGTTTGTATGATATTCCTGTGCGATGAGTTTGGAGCTGGGTTAAATATCTAAGAAATATACAT 739
Db 678 AGCATATATGACATACCAAGCCGATGAGTTTCGGGCGGCACCTCTTGAGGAAAAATGTCCAT 737
Qy 740 GTATGTTATGAGCTTCCATTTTGGCAAGCAATATTTACTAGACCGAGCGGTTACG 799
Db 738 ACGTGTATGCGCTTTTCCATCTCTCGAAGCCTGCTTCTTGAAGATTCATACGTCAAT 797
Qy 800 CTTAATGAAATAGGCGCAACTTTCAAAGAGAAAGTGATGATGTTCTTTTCTTTTCTTTGCT 859
Db 798 TTGGACGAAATCAACGCGTGTCTTTCGCGCATGGAGACAAGTTGACCTTTCTTTTGA 857
Qy 860 GATGAAGTACTTTAAATATATAGTCATAAATACAAAATATCTTGCATATGTAGTTAAA 919
Db 858 TCAGAGAGTACTTTAAATATATGTATAGTTATTTCTAATATCTTAAAGTATGTGTCAAA 917
Qy 920 TCTTACTTTCTGCTTCTAGTAGAATAGTTTACTTTTAAAGGAATTTTGTAGTCACTAGGGTT 979
Db 918 ACTTACTTCCGGCTCTAATAGAGAGTTTACATGAAGAGTTTGTAGTCCACAGATT 977
Qy 980 AATACCTGGTTTGTAAATTTACAAAGTAGATACCTATATTTCTGTACAAGAGTTGTAGA 1039
Db 978 AATACCTGGTTTGTAAAGTTTCTAGAAATAGATACTTTTCTTTTGTACAAAGGTGTGCC 1037
Qy 1040 CAAGTAGGGTGTATAGTAGTACGTTCTATAGAGGGATGGAAGACGCTTGTCTTACAG 1099
Db 1038 CATAAAAGTGTAGATAGTACAGCTTTTATATCTGCAATGGAAGACGCTGCGCATTAACAA 1097
Qy 1100 AAAACCTTGGCCATGTTTCAACACATGAAGAGCAATCTTTAGAGACAGCGCTTCGGTTAAC 1159
Db 1098 ANGACTCTTGCAATGTGCACAGCAGAGAAATCTCTTGTAGGATTCATCATCAGTCAAT 1157
Qy 1160 TTTTGGTTTCCCTAAGATGAAGGACATGTTGATAGTACGCTGTTTGTAGGGTTCCTATTACC 1219
Db 1158 TACTGGTTTCCAAAATGAGGGATATGTCATCGTACCATTATTTCGACATTTCTTTGGAG 1217
Qy 1220 AGCAAAAGATGACAGAGGTGAGGTCAATGTTTAAATCGTGACTTCGTTTACAGAGTGT 1279
Db 1218 ACTAGTAGAGGCGCGCAAGGAAATCTTAGTGTCCAAGGATTTCTGTTTACAGTGTCT 1277
Qy 1280 AATCATATCAACATATCAAGCCAAAGCGTTAACTTACAGAACGTTATTTCTTCTG 1339
Db 1278 AACCACATTCGAACATACCAGCGAAGCTCTTACATACGCAATGTTTGTCTTTTGTCT 1337
Qy 1340 GAGTCTATAAGATCCCGGTGATTAATCAATGGTGTACTGCTAGGTCTGAAATGGGATGTA 1399
Db 1338 GAATCGATTGCGATCGAGGTAATCATTAACGTTGTGACAGCGAGTCCGATGGGATGTG 1397
Qy 1400 GATTAAGCAATCTTTCAACCTTGTCAATGACTTTCTTCTTGTGAGACTTAAGCTGGCTGCG 1459
Db 1398 GACAAATCTTTGTTACAACTCTGTCCATGACGTTTACCTGTCATCTAAGCTTTGCCGTT 1457
Qy 1460 CTTCAAGACGATATAGTAATGGGAAAGTTTTCGGTGTCTGGATAAGACACCTTCTGAACT 1519
Db 1458 CTAAGGATGACTTACTGATTAAGCAAGTTTGTAGTCTCGGTTCCGAAACGGTGTGCCAGAT 1517
Qy 1520 ATTTGGGATAGGTGGGCAATTTTTTGGAAACGTTTTTCCCACTATCAAAAGAGAGATTG 1579
Db 1518 GTGTGGGATGAGATTTTCGCTGCGGTTTGGGAAACGCAATTTCCCTCCGTGAAAGAGAGGCTC 1577
Qy 1580 GTGACAGGAAAAATCTGGATGTAAGTCAGAAATGCTCTGAGATCAAGATCCAGATCTG 1639
Db 1578 TTGAACAGGAAATTTATCAGAGTGGCAGCGACCATTTAGAGATCAGGGTCCCTGATCTA 1637
Qy 1640 TATGTACATGGAAGACAGGTTCGTAGCTGAATACACCAAGTCTGAGGAGTTTACCGCAT 1699

Db 1638 TATGTGACCTTCCACGACAGATTAGTACTGAGTACAAGGCTCTGTGGACATGCCTCG 1697
Qy 1700 CTAGATATCAAGAAAGGACTTAGAAGAAAGCTGAGCAAAATGTACAGCGGTTATACGAATTA 1759
Db 1698 CTTGACATTAGGAAGAAGATGGAAGAAACGGAAGTGTATACAATGCACTTTCAGAGTTA 1757
Qy 1760 TCTATCCTTAAGGCTGCTGATTAATTTTCGATATCGGAAGTTTCAAGACATGTCGAAGCT 1819
Db 1758 TCGGTGTTAAGGGAGTCTGCAAAATTCGATGTGTATGTTTTTCCAGATGTGCCAATCT 1817
Qy 1820 TTAGATGTAGTCTGATGTGGCAGCAGAGTAATCTGTGAGTGGCGGCGAGAAATAGAAC 1879
Db 1818 TTGGAAGTTGACCAATGACGCGACGGAAGTTATAGTTCGGGTTCATGAGCAATGAGAGC 1877
Qy 1880 GGTTTAACTCTTACTTTTGTATAGCCAAACCGAGAGAAATGTGGTAAAGCTCT-----T 1933
Db 1878 GGTCTGACTCTCACTTTGAAACGACCTTACTCAGCGCAATGTTGCGCTAGCTTTACAGGAT 1937
Qy 1934 AAAAGCAGCGGCTCTGAGCGCGTGGTATGCTTGAACCGACATCCGAAGAGGTGAACGTA 1993
Db 1938 CAAGAGAAGGCTTCAGAAGGCTGCTTTGGTAGTTTACCTCAAGAGAAGTTGAAAGAACCGTCC 1997
Qy 1994 AATAAAATTTTCTATTGCTGAGAAAGGAGATTGCTCTGTGTGCGAGAAAGTCATGTTTG 2053
Db 1998 ATGAAGGTTTCGATGGCCAGAGGAGATTACAATTTAGCTGCTTGTCTGGAGATCATCCG 2057
Qy 2054 ACGAATGCTAACTTAGAGCACAGGAGTTGGAGTCCCTCAACGATTTCCATAAGGCTTGC 2113
Db 2058 GAGTCGTCTTATTCTAAGAACGAGGAGATAGTCTTTTAGAGCAGATTTCATATGGCAACG 2117
Qy 2114 GTGATAGTGTGATTAACAAGCAATGGCATCGGTTCTCTACACTGGCTCACTCAAGATT 2173
Db 2118 GCAGATTCGTTAAATTTCTGAAGCAGATGAGTCTGATGTTGTACACGGGTCCGATTAAAGTT 2177
Qy 2174 CAACAAATGAAGAACTATGTGGACAGTTTGGCAGCTTCGTTGTCCGACATGTATCAAA 2233
Db 2178 CAGCAATGAAGAACTTTATCGATAGCTGGTAGCATCATATCTGTGCGGTGTGCAAT 2237
Qy 2234 CTATGCAAGTCACTPAAAGGATGAAGTCGGGTATGATTTCTGATTCAGGGAGAAAGTTGGT 2293
Db 2238 CTCGTCAAGATCTCTCAAGATACAGCTGCTATTGACCTTGAAACCCGCTCAAAAGTTTGA 2297
Qy 2294 GTTTGGATGCTACTTTGAAAAAGTGGCTCCTCAAACTCGCGCAAGGTCATTCATG 2353
Db 2298 GTCTTGGATGTTGATCTTAGAAGTGGTTAATCAACCAACGCGCAAGAGTCATGCTG 2357
Qy 2354 GGAGTGTCTCTGGATTACAAGGGGAAAAATGTTTACTGCACTTCTATCTTATGAAGAGAT 2413
Db 2358 GGTGTTGTTGAAACCCACGCGAGGAAGTATCATGTGGGCTTTTGGAAATATGATGAGCAG 2417
Qy 2414 AGAATGTGATCTGAGACGACTGGAGAGGGTGGCTGTATCATCTGTATACAAATGGTATAT 2473
Db 2418 GGTGTGTGATCGGATGATTTGGAGAAGTAGTCTGTCACTCTGAGTCTGTGTTTAT 2477
Qy 2474 TCTGATATTCGAAGCTCCAAATCTCAGGAAACAAATGAGACGCTGAAACCCACGAA 2533
Db 2478 TCCGACATGGCGAACTCAGAACTCTCGCAGACTGCTCGAAACGGAGAACCCGATGTC 2537
Qy 2534 CCTACTCAAGATGTTGTTGTTGAGTGGGCTGCTGTTGTGTGAAAGTACAAAGGAGAT 2593
Db 2538 AGTAGCGCAAGGTTGTTCTTGTGACGAGTTTCCGGGCTGTGGGAAAAACCAAGAAAT 2597
Qy 2594 TTTGAAAGATTTGATCTTGTAGAGGATTTGATCTTGGTTTCTTGAAAAACAAGCTGCTGCT 2653
Db 2598 CTTTCCAGGGTTAATTTTGTATGAAGATCTAATTTTAGTACCTGGGAAACGAAGCCCGGAA 2657
Qy 2654 ATGATCAGAGAAGGGCTAATCTCATCTGACTAAGAGCCAAATGGAACAATGTGAGA 2713
Db 2658 ATGATCAGAGAAGCTGCAATTTCTCAGGGAATTTGTGGCCACGAAGGACAAAGTTAAA 2717
Qy 2714 ACGTAGATTCACTTCTTAATGTCAT-----CCAAAAACCGGATCACACAAGAGGCTT 2764
Db 2718 ACCGTTGATCTTTTCATGATGAATTTTGGGAAAGCACAGCTGTGAGTTCAAGAGGTTA 2777

QY 2765 TTTATTGATGAAGGTTGATGCTGCACACCGGTTGTGTAACTTCTCGTGTCTATCTCT 2824
DB 2778 TTCAITGATGAAGGTTGATGTTGCATCTACTGTTGTGTAAATTTCTTGTGGCGATGCA 2837
QY 2825 GGTTCGCACATCGCATACATTTACCGAGATACACAGCAGATCTCTTTTCAATTAACAGATT 2884
DB 2838 TTGTGCGAAATTCATATATGTTTACCGAGACACACAGCAGATTCCTATACATCAATAGATT 2897
QY 2885 CAGAAATTTCCCGTATCCCAAAACATTTTGAGAGCTGCAAGTGGATGAAGTTGAGATGAGG 2944
DB 2898 TCAGAAATTCCTCGTATCCCGCCCATTTTGCCAAATTTGGAAGTTGACGAGGTGGAGACACGC 2957
QY 2945 AGGACACACTGAGATGCGCCAGGTGATGTGAATTTTCTTCAATTCGAATGCAAGGA 3004
DB 2958 AGAACTACTCTCCGTTGTCAGCCGATGTACACATTTATCTGAAACAGGAGATATGAGGCG 3017
QY 3005 GCGGTGACAAACACCTTCAACTGTCAACGATCGGTCTCATCTGAGATGATAGGCGGTAAAG 3064
DB 3018 TTTGTATGAGCACTCTCTCGGTTAAAGATCTGTTTCGACGAGATGGTTCGCGCGAGCC 3077
QY 3065 GGAGTACTAAACAGTGTTCCTCAACCACTTAAAGGGAATTTGTAACCTTCACTCAGGCT 3124
DB 3078 GCGGTGATCAATCCGATCTCAAAACCCCTTGCAATGGCAAGATCCTGACTTTTACCCCAATCG 3137
QY 3125 GATAAATTTGAGTTAGAGAGAGGCTTAAAGATGTGAACACACCGTTTCATGAGATCCAA 3184
DB 3138 GATAAAGAGCTCTGCTTCAAGAGGATTTACAGATGTCACTGTGATGAAGTGCA 3197
QY 3185 GGAGAAACCTTTGAAGATGTGCTGCTGTCAGATTGACGGCAACTCCACTGACTCTGATT 3244
DB 3198 GCGGAGACATCTCTGATGTTTCACTAGTTAGGTTAAACCCCTACACCACTCTCCATCAAT 3257
QY 3245 TCCAAGTCTTCCCGCATGTTCTAGTCGCTCTGACTAGACACACAAAGAGCTTCAAAATAT 3304
DB 3258 CGAGGAGACAGGCCCATGTTTGTGTCGATTTGTCAAGGCAACCTGTTTCGCTCAAGTAC 3317
QY 3305 TACACGTAGTTAGATCTTTTAGTACAGATAATTTAGTGAATTTGTCTTTTAAAGCTCC 3364
DB 3318 TACACTGTTGTTATGATCTTTAGTTAGTATCAATTAGAGATCTAGAGAACTTAGCTCG 3377
QY 3365 TTCTTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3424
DB 3378 TACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3437
QY 3425 GTGTTCAAAGGTCATATCTCTTTGTGGCAACACCTTAAATCAGGAGACTTTCCAGATCTA 3484
DB 3438 GTGTTCAAAGGTTCCAAATCTTTTGTGTCGATTTGTCAAGGCAACCTGTTTCGATATG 3497
QY 3485 CAGTTCTATTACGATGATGCTCCCTCGTGAATAGTACTTAAACAGTATGATGCT 3544
DB 3498 CAGTTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3557
QY 3545 GTTACCATGAGTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3604
DB 3558 GTTACCATGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3617
QY 3605 AAAAGTATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3664
DB 3618 AAGTCTGTTGCTCGCTTAAGGATCAAAATCAAAACCACTAATACCTATGTTAGTACGAAACGGG 3677
QY 3665 GCGAACCCGAGGCTGCGAGCTACTCGAAATCTGTTGCAATGATTAAGAAAT 3724
DB 3678 GCAGAAATGCGCCAGACTGAGCTATTTGGAATTTTATGTCGAGATTAAGAAAT 3737
QY 3725 TTCAACGACACCACTGACGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3784
DB 3738 TTTAAAGCAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3797
QY 3785 GATAAGTTTTCATAGCTATTTTATTAAGAAAGAAATACACAAATAATTTGCTGGA 3844
DB 3798 GATAAGTTTTCATAGCTATTTTGTAAAGAAAGAAACCAATATAATTTTCTCT 3857

QY 3845 GTGATGACGAAGGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3904
DB 3858 TTGTTAGTAGAGAGCTCTCTCAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3917
QY 3905 GACTTGGCTAACTACAATTTTACAGATCTCGCGCCATCGATCAAGTCAAGCAACATGATC 3964
DB 3918 CAGCTCGCAGATTTGATTTGTAGATTTGCGCAGCTGATCAGTACAGACACATGATT 3977
QY 3965 AAGGCTCAACCAAAACAGAAATTTGGAATTTCAATTCAGATGAATACCTGCTCTGCA 4024
DB 3978 AAAGCACAACCAAGCAAAATTTGACACTTCAATCCAAACGGAGTACCCGCTTTGCG 4037
QY 4025 ACAATTTGCTACCATTCGAACGATCAACGATTTTGGCGGTTTCTCA--GAGCTT 4081
DB 4038 ACGATTTGTTACCATTTCAAAAAGATCAATGCAATTTTGGCCCTTTGTAGTGAGCTT 4097
QY 4082 ACAAGTTGCTGCTCGAGGCTTTGATTTCTAAGAAATTTCTTTTCTTACTAGGAAAATCT 4141
DB 4098 ACTAGGCAATTTACTGGCAGTGTGATTTGAGCAGATTTTGTGTTTTCACAAGAAAGACA 4157
QY 4142 CCAGAACAGATTTCAAGAAATTTTCTCGGATCTCGACTCGCAGTTCTTATGATGTGTA 4201
DB 4158 CCAGCGCAGATTTGAGGATTTCTTTCGAGATCTCGACAGTCTGTCGCGATGATGATGCTTGT 4217
QY 4202 GAACTGGATTTTCTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4261
DB 4218 GAGCTGGATATATCAAAATACGACAAATCTCAGAAATGAAATTCACCTGTCAGTAGAATAC 4277
QY 4262 GAAATATCGAAAGATTCGGTCTCAATGATTTTGGCGGAGTGTGGAACCAAGGGCAC 4321
DB 4278 GAGATCTCGCGAAGATTTGGTTTTGAGACTTCTTGGGAGAGTTTGGAAACAGGGCAT 4337
QY 4322 AGGAAAAACAATTTTCAAGGATTTACATTTCTGGAATCAAGACATGCTGTGGTATCAAAAG 4381
DB 4338 AGAAGAACCACTCTCAAGGATTTATACCCGAGTATAAAAACTTGATCTGGTATCAAGA 4397
QY 4382 AAAAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4441
DB 4398 AAGAGCGGGAGCTCAGCAGCTTCAATGGAACACTGTGATCAATTTGTCATGTTTGGCC 4457
QY 4442 TCAATTTTACCGATGAAAGGTCATAAAGGTGCTTTTGTGGAGACGATTCGCTTTTG 4501
DB 4458 TCGATGCTTCCGATGAGAAATATCAAGAGGCTTTTGGGTGACGATGATGCTGCTG 4517
QY 4502 TATTTTCCAAAGGTTTGGATTTCCCTGACATTTCAAGTCAATGCTGTAATCTCATGTGGAAT 4561
DB 4518 TACTTTCCAAAGGTTTGGATTTCCGCGATGTGCAACACTCCGCGAATCTTATGTGGAAT 4577
QY 4562 TTTGAGGCCAACTCTGTATGAAAGGATACGGTTACTTTTGTGGTAGATACATCATAC 4621
DB 4578 TTTGAAGCAAACTGTTTAAAAAACAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 4637
QY 4622 CATGATAGGAGCAATAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4681
DB 4638 CAGCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4697
QY 4682 AAACATATCAAGGATTTATGATCACTTAGAAGATTAAGGTTGCTTTTGTGCGATGTTGCT 4741
DB 4698 AAACATATCAAGGATTTGGAACACTTTGGAGATTCAGAAAGTCTCTTTGTGATGTTGCT 4757
QY 4742 TGTTCGCTCGAAACTGTTGCTTTCCGAGCTTTCGAGCTGAAACGAGCTATCAAGGAGTT 4801
DB 4758 GTTTCGTT--GAACAATTTGCTGATTTACACAGATTTGAGACGCTGTATGAGGAGTT 4814
QY 4802 CATAAACCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4861
DB 4815 CATAGACCGCCCTCCAGGTTGCTTTTATTAAGGTTCTGGTGAAGTATTTTGTCTGAT 4874
QY 4862 AAATTTTATTTAGAACTTTGTTTTTAAATGCTGTTAGTCTCAGAGATGATGATGATGATGATGAT 4921
DB 4875 AAAGTCTTTTGAAGTTTGTGTTTATAGATGCTCTAGTTGTTTAAAGGAAAGTGAATAT 4934
QY 4922 TAGCGAGTTCAATGATCTTTTCGAAACAGGATGAGATATCTTCGCGCATTCATGACTAAGGT 4981

Db 4935 CAATGAGTTTATCGACCTGACAAATAATGGAAGATCTTACCGTCGATGTTTACCCCTGT 4994
Qy 4982 CAAGAGTGTAGAAATATCGACTGTGGACAAGATATATGCTGTGTTAAGAATGATAGTCTTTTC 5041
Db 4995 AAAGAGTGTATGTGTTCCAAAGTTGATAAATAATGTTTCATGAGATGATGATCTGTC 5054
Qy 5042 TGATGTAGATTACTTAAAGGTGTTAAGTTAGTTAAGAAAGGATATGTCCTTAGCTGA 5101
Db 5055 AGAGGTGAACCTTCTTAAAGGAGTTAAGCTTATTGATAGTGATACGTCCTGTTAGCCGG 5114
Qy 5102 TTGTGTAGTGTGCGGAGTGGAACTCCCGGATAACTCCGTCGTGTCGTGTCAGTGTG 5161
Db 5115 TTGTGTCTCAGGGCGAGTGGAACTCCCTGCAATTCGAGAGAGGTGAGCGGTG 5174
Qy 5162 TATTGTAGATAAGAGAATGAAGGAGTGAAGGAAGCAACGCTGGGTGGTATACGCCCC 5221
Db 5175 TCTGTGACAAAAGGATGGAAGAGCGACGAGGCCACTCTCGGATCTTACTACACAGC 5234
Qy 5222 TGCTTGCAAAAGAAATTTTCTTTTAAGCTAATCCCTAATTTTCAATAAATATCGGAGGA 5281
Db 5235 AGCTGCAAGAAAGAAATTTTCAAGTTCGTTCAAGTTCGTTCCCAATTTATGCTATAACCAACCCACGA 5294
Qy 5282 TGCTGAGAACGACCGCTGCGCAAGTGTAGTGAATATCAAGAGTGGCTATGGGAAGG 5341
Db 5295 CGGATGAAACGCTCTGGCAAGTTTATGTTAATATAGAAATGTGAAGATGTGACGGG 5354
Qy 5342 ATACTGTCCTTTATCTTTGAGAGTTCGTTTCAATTTGTGTAGTACATAAAATAATGTAAG 5401
Db 5355 TTCTGTCGCTTCTCTGGAGTTGTGTCGCTGTGTTATGTTTATAGAAATAATATAA 5414
Qy 5402 AAAAGTTTGAAGGAACGATTTTGAAGTGTGACAGACGCTCGCAATTTGAACCTCACTGA 5461
Db 5415 ATTAGTTTGAAGAGAAGATTACAAACCTGAGAGACGAGGCGCCATGGAACCTTACAGA 5474
Qy 5462 AAAGTGTGTCAGAGTTCGTTGGATGAGTACCAATCGCTGTAACCTCGAAAGGTTTC- 5520
Db 5475 AGAAGTCTTATGAGTTCATGGAAGATGTCCTTATGTCGATCAGGCTTGCAAAAGTTTCG 5534
Qy 5521 -----CGAAACAAAGAAATGTTAGTGAATATGTTAATAAT----- 5561
Db 5535 ATCTCGAACCGAAAGAGATGATGTCGCAAGGGAATAATAGTATGATCGGTC 5594
Qy 5562 -----AAGAAATAAATACAGTGTGAAGAGGTTTAAATATGAGGAATTTAGGA 5614
Db 5595 AGTCCGAACAAGAACTATAGAAATGTTAAGGATTTTGAGGAATGAGTTTAAAGAA 5654
Qy 5615 TAATGTAAGTGTACACGAGT-----CTATCGCTCATCGAGTACGTTTATCAAT 5665
Db 5655 TAATTAATCATGATGATGATTCGGAGGCTACTGTCCCGAATCGGATTCGTTTTA- 5711
Qy 5666 ATGCTTATACAACTCACTCCGAGCCAAATTTGTTTATCTTATCTTCGCTTACGCGAGAT 5725
Db 5712 ATGCTTACAGTATCACTACTCTCATCTCAGTTCGTTGTTCTGTCATCAGCGTGCGCGAC 5771
Qy 5726 CCGTGCAGCTGATCAATCTGTGTACAAATGATGATGGTATACAGTTCATCAACCGCAAA 5785
Db 5772 CCAATAGAGTTAATTAATTTATGTAATAATGCCTTAGGAATTCAGTTTCAACCAACAA 5831
Qy 5786 GCTAGGACAAACAGTCCCAACACAAATTCGCGATGCTCGGAAACCTGTGCTAGTATGACA 5845
Db 5832 GCTGAACTGCTGTTCAAAGCAATTCAGTGGGTGGAACCTTCCACCAAGTAACT 5891
Qy 5846 GTGAGATTTCTGCTCGGATTTCTTATGTGTATAGATATAATTCGACCTTTGATCCGTTG 5905
Db 5892 GTTAGTTCCCTGACAGTGACTTTAAGGTGTACAGGTACATGCGGTATTAGACCCGCTA 5951
Qy 5906 ATCAGCGGTTTATTAATAGCTTTGATCTAGAAATAGAAATAATAGAGTTGATTAACAA 5965
Db 5952 GTCACAGCACTGTTAGGTGCAATTCGACACTAGAAATAGAAATAATAGAGTTGAAATCAG 6011
Qy 5966 CCGCAGCCGAATACTACTGAAATCGTTAAACCGACTCAGAGGTTAGACGATGCTACTGTA 6025

Db 6012 GCGAACCCAGCACTCCGAAACGTTAGATGCTACTGTTAGAGTAGACGACGACCGTG 6071
Qy 6026 GCTATAAGGGCTTCAATCAATAATTTGGCTAATAAGAACTTGGTTCTGGAACTGGCATGTC 6085
Db 6072 GCCATAAGGAGCGGATAAATAATTTAATAGTAAATTTGATCAGAGGAACCGGATCTTAT 6131
Qy 6086 AATCAAGCAGGCTTTGAGACTGTAGTGGACTTGTCTGGACCAACAATCCCGCTACTTAG 6145
Db 6132 AATCGAGCTCTTTTCGAGAGCTCTTCTGGTTTGGTTTGGACCTCTGGTCTCTGCAACT- 6188
Qy 6146 CTATTTGTTGAGATTTCTTAAATAAAGTCGCTGAAGACTTAAATTCAGGGTGGCTGA 6205
Db 6189 -TGAGGTAGTCAAGATGCAATAATAAATACGGATTGTTCGTTAATCACA-CGTGGTGG 6246
Qy 6206 TACCAAAATCAGCAGTGGTTTTCGTCACCTTAAATATAACGATTTGTCATATCTGGATCC 6265
Db 6247 TACGATAACGCATAGTGTTCCTCCCTCACTTAAATCGAAGGGTTGT-GTCTTGGATCGC 6305
Qy 6266 AACAGTTAAACCATGTGATGGTGTATGCTGTTATGCTGATGCGTAAACATCGAGAGGTTCCG 6325
Db 6306 GCGGGTCAAAATGTATATGTTTCATATACATCCGACGACGTAATAAAGCGAGGGTTTCG 6365
Qy 6326 AATCCTCCCTAAACCGCGGTAGCGGCCCA 6355
Db 6366 AATCCCGCTTACCCCGGTAGGGGCCCA 6395

RESULT 5

US-09-962-527-2

; Sequence 2, Application US/09962527

; Publication No. US20030049813A1

; GENERAL INFORMATION:

; APPLICANT: GARGER, STEPHEN

; HOLTZ, R. BARRY

; McCULLOCH, MICHAEL

; TURPIN, THOMAS

; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND

; PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES

; FROM PLANT SOURCES

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Howrey & Simon

; STREET: 1299 Pennsylvania Avenue N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/962,527

; FILING DATE: 24-Sep-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/037,751

; FILING DATE: 10-march-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Halluin, Albert P

; REGISTRATION NUMBER: 25,277

; REFERENCE/DOCKET NUMBER: 00801.0140.999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-463-8109

; TELEFAX: 650-463-8400

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6439 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

Db 1038 CAUAAAAGUGAUGAGCAGCUUUUAUACGCAUAGGAAGCGCAUGCAUUAACAA 1097
Qy 1100 AAAACCTTGGCGATGTTCAAACCTGAAAGAGCAATCTTTAGAGACACGGCTTCGGTTAAAC 1159
Db 1098 AAGACUCUUGCAUUGUGCAACAGCAGAGAAUCCUCCUUGAGGAAUUAUCAUCAUGCAU 1157
Qy 1160 TTTTGGTTCCTAAGATCAAGACATAGTGTATAGTACCGCTGTTTGAGGGTCTTATTACC 1219
Db 1158 UACUGUUUUCCAAAAGGGAUGUGUACUGAACCAUUAUUCGACAUUUUUUGGAG 1217
Qy 1220 AGCAAAAAGATGACAAGAGTGAAGTCAATCTGTAATCTGTACTGCTAGGTCGAATGGATGTA 1279
Db 1218 ACUGAUGAGGACCGCGCAAGAGUCUUAUGUCCCAAGAUUUCUGUUUAACAGUGCU 1277
Qy 1280 AATCATATCAGAACATATCAAGCCAAAGCGTTAACTTACCAGAAACGTAATATTCTTTCGTG 1339
Db 1278 AACCACAUUCGAACAUACCGAGCGAAAGCUCUUAUCAUACGCAAAUUGUUUUGUCCUUGUC 1337
Qy 1340 GAGTCTATAAGATCCCGGTGATTAATCAATCGTGTACTGCTAGGTCGAATGGATGTA 1399
Db 1338 GAUUGCAUUCGAGGAGGUAUAUUAACCGGUGACAGCGAGGUCGGAUUGGAGUG 1397
Qy 1400 GATAAAGCAATCTTCAACCCCTGTGCAATGACTTCTTCTTTCGACACTAAAGCTGGCTGCG 1459
Db 1398 GACAAAUUCUUGUAACAUCUUGUCCAUAGCGUUUAUCUGCAUUAUAGCUUGCCGU 1457
Qy 1460 CTTCAAGACGATATAGTAAATGGGAAGTTTCGGTGTCTTGGATAGACACATCTTGAACCTT 1519
Db 1458 CUAAAAGGAUGACUACUGAUAGCAUUUAUGUCUGGUUUGCAAAACCGGUGCGACGAU 1517
Qy 1520 ATTTGGGATGAGTGGGCAAAATTTTGGAAACGTTTCCCACTATCAAGAGAGATTG 1579
Db 1518 GUGUGGAUGAGAUUUCUGCGGCUUUGGGAACCAUUCUCCUGGGAAGAGAGGCCUC 1577
Qy 1580 GTGAGCAGGAAATCTCGATTAAGTGAGAAATGCTCTGAAGATCAAGATCCAGATCTG 1639
Db 1578 UUGAACAGGAAACUUAUCAGAGUGCGCAGCGCAUUAUAGAUACAGGUGCCUAGAU 1637
Qy 1640 TATGTACATGGAAGACAGTTTCGTAGCTGAATACACCAAGTCTGAGGAGTTACCGAT 1699
Db 1638 UAUGUGACUUCACGACAGAUAGUGACUGAUACAAGGCCUCUGUGGACAUUGCCUGCG 1697
Qy 1700 CTAGATATCAGAGGACTTAGAAGAGCTGAGCAATGTACGACGCGTTATCAGATTA 1759
Db 1698 CUUGACUUAUGGAAGAAGUAGAAACGGAAGUGAUGAUAUUGCAUUCUACAGAU 1757
Qy 1760 TCTATCTTAAAGGTGCTGATAATTCGATATCGCAAGTTTCAAAAGACATGTCAAGGCT 1819
Db 1758 UCGGUGUUAAGGAGUCUGACAAAUUCGAUUGAUUUUUUCCAGAUUGGCCAUUCU 1817
Qy 1820 TTAGATGTTAGTCTGTGATGGCAGCAGAGTAATCTGTTGAGTGGCGGAGAAATAGAGC 1879
Db 1818 UUGGAAGUUGACCCAAUAGACGCGAGGAAGUUAUAGUCGCGUACAGGACAAUAGAGC 1877
Qy 1880 GGTTTAATCTTACTTTTGATAAGCCACCGAGAGATGTGGCTTAAGGCTCT-----T 1933
Db 1878 GGUCUGACUCUCAUUAUGAACGACCUACUGAGCGAAUUGUUGCGUACUUUAACAGGA 1937
Qy 1934 AAAAGACGGCGTCTGAGCGCGTGTATGTCTTGAACCGACATCCGAAGAGGTCAACGTA 1993
Db 1938 CAAGAGAGGCUUCAGAGGUGCUUUGUAUGUUAUCCUACAAGAAUUGAAGACCGGUCC 1997
Qy 1994 AATAAATTTTCTATTTGCTGAGAAAGGAGATTGCTGTGTGTGAGAAAGTCTATGGTTTG 2053
Db 1998 AUGAAGGUGUUGAUGGCCAGAGGAGUUAUUAUAGUGUGUCUUGUGGAGAUCAUCCG 2057
Qy 2054 ACGATGCTAATCTAGACACAGAGTTGGAGTGGCTCCCTCAACGATTTCCATAAGGCTTGC 2113
Db 2058 GAGUGUCUUAUUCUUAAGAAACGAGAGAUAGAGUCUUAUAGAGCAGAUUAUAGCAACG 2117
Qy 2114 GTGGATAGTGTGATTAACAAAGCAATGGCATCGTGTGTCTACTGCTCACTCAAAAGTT 2173
Db 2118 GCAGAUUCGUUAUUCGUAAGCAGUAGAGCUGGAUUGUUAUACACGGGUCCGUAUUAAGU 2177

Qy 2174 CAACAAATGAAGAACTATGTGGACAGTGTGGCAGCTTCGTTGTCCGCCACTGTATCAAT 2233
Db 2178 CAGAAAUGAAAAUUUUUCGAUAGCUGGUAAGCAUUAUCUGCGUGGUGCGAUA 2237
Qy 2234 CTATGCAAGTCACTTAAAGGATGAAGTGGGTATGATTCTGATTCAGGGAGAAAGTTGGT 2293
Db 2238 CUCUGAAGAUCUCCAAGAUAACAGCUGUAUUAUCCUUGAACCUGCAUAAAGUUUGGA 2297
Qy 2294 GTTTGGGATGCACTTTTGAAGAAAGTGGCTCTCTCAAACTCGCGGCAAGGTCATTCTATGG 2353
Db 2298 GUCUUGAUGUUGCAUCUAGAGAGUGGUUAUAUCAAACCAAGCGCAAGAGUCAUGCAUG 2357
Qy 2354 GGAGTTCTCTGGATTAACAAGGGGAAAATGTTTACTGCATCTTCTATCTTATGAAGAGAT 2413
Db 2358 GGUGUUGUAGAAACCCACGCGAGGAUUAUCAUGUGCGCUUUUGGAUAUAGUAGAGCAG 2417
Qy 2414 AGAATGCTGACTGAGACGACTGGAGGAGGTGCTGTATCATCTGTATACATATGATATAT 2473
Db 2418 GGUGUGGAGCAUGCGGAUUAUGGAAGAGUAGCUCGACGUCUGAGUCUUGUUGUUU 2477
Qy 2474 TCTGATATTCGAAAGCTTCCAAAATCTGAGGAAAAACAATGAGAGACGGTGAACCCCAAG 2533
Db 2478 UCCGACAUGCGGAAACUCAGAACUCUCUGCGCAGACUGUCUUGAAGCGAGAACCGCAUGUC 2537
Qy 2534 CCTACTCAGAGATGTTGATCTTTGGATGGGTGCTGTTGTGGAAGAGTACAAAGGAT 2593
Db 2538 AGUAGCGCAAAAGGUGUUCUUGUGGACGGAUUCGGGUGUGGGGAAAAACCAAGAAAU 2597
Qy 2594 TTTGAAAGATTGATCTTTGATGAGGATTTGATCTTTGCTCTGAAAAACAGCTGTGCT 2653
Db 2598 CUUCCAGGGUUUAUUUGAUGAAGAUUAUUUUUAGUCCUGGGAAGCAAGCCCGGAA 2657
Qy 2654 ATGATCAGAAAGAGGGCTAATCTCTGGACTGATAAGAGCCACAATGGACAATGTGAGA 2713
Db 2658 AUGAUCAGAGAGCGUGGAAUCCUCAGGAAUUAUUGUGCCACGAAGGACAACGUUAAA 2717
Qy 2714 ACGGTAGATTCATCTTAAATGCAATCCAAAACCGCGATCACA-----CAAGAGGCTT 2764
Db 2718 ACCGUGAUUCUUUAUGAUGAAUUUUUGGAAAAACACGCGUCUGACUUAUAGAGU 2777
Qy 2765 TTTATTATCAAGGGTTGATGTGCACACCGTGTGTGTTAACTTCCTGGTCTTATCTCT 2824
Db 2778 UUCAUUGAUGAAGGUUGAUGUUGCAUUCUGUUGUUGUUAUUUUUUGUGCGCAUGUCA 2837
Qy 2825 GGTTCGACATCGCATACATTTACGGAGATACACAGCAGATTCCTTTTCATTAAACAGATT 2884
Db 2838 UUGUGCAAAUUGCAUUGUUUACGGAGACACACAGCAGAUUCCAUACAUAUAGAGU 2897
Qy 2885 CAGNATTTCCGTTATCCAAAACATTTTGAGAGCTGCAAGTGGATGAAGTTGAGATGAGG 2944
Db 2898 UCAGGAUUCGUAACCCGCCCAUUUUUGCCAAAUUGGAAGUUGACGAGGUGGAGACGC 2957
Qy 2945 AGGACACACTGAGATCCAGAGTGATGTGAATTTTTTCTTACAAATCGAAGTACGAAGGA 3004
Db 2958 AGAACUAUCUCCGUUGUCCAGCGCAUGUCACAUUAUCUAGAACACAGAGAUUAGAGGC 3017
Qy 3005 GCGGTGAACAACCTTCAACTGTAAACGATCGGTCTCATCTGTAGATGATAGCGGTAAG 3064
Db 3018 UUUUGAUGAGCACUUCUCGUUUAUAAAGUCUUGUUGCGAGGAGAUUGCGCGGAGCC 3077
Qy 3065 GGAGTACTAAACAGTGTTCCAAACCACTAAAGGGAAAATTTGTAATTTTCACCTCAGGCT 3124
Db 3078 GCCGUGAUCAUCCGACUCUCAAACCCUUGCAUGGCAAGAUCCUGACUUUUAACCAUUG 3137
Qy 3125 GATAAATTTGAGTTAGAGGAGAGGGCTATAAGAAATGTGAACACCGTTCATGAGATCCAA 3184
Db 3138 GAUAAAGAGCUCUCUGUUUACAGGGGUUAUUCAGAUUUCACACUCUGCAUGAAGAGCAA 3197
Qy 3185 GGAGAAACCTTTGAAGATGTGTGCTGGTCAAGTTGACGGCAACTCCACTGACTCTGATT 3244
Db 3198 GCGGAGACAUAUCUCUGAUGUUUACUAGUUAAGGUUAAACCCCAACACGAGCUCUCAU 3257

Db 5415 AUUAGGUUUGAGAGAGAAUUAACAAGUGAGAGACGGAGGCCCAUGGAAUUAACAGA 5474
Qy
Db 5462 AAAGGTTGTTGAGGAGTTCTGGATGAAGTACCAATCGCTGTGAAACTCGAAAGGTTCC 5521
Db 5475 AGAAGUCGUUGAGUUGAUGGAAGAUGUCCUUAUGCAUGACGCGUUCGAAAGUUCG 5534
Qy 5522 GG-----AAAACAAAAGAAATGGTAGGTAAATGTTTAAT----- 5561
Db 5535 AUCUCGAACCGGAAAGAGUGAUGCCGCAAGGGGAAAUAGUAGUAAUGCUGUC 5594
Qy 5562 -----AAGAAATAATAACAGTGTGAAGGGGTTTAAATTCAGGAAATTGAGGA 5614
Db 5595 AGUCCGACACAGACUAUAGAAUUGUUAAGGAUUUUGGAGGAUAGUUAUUAAGAA 5654
Qy 5615 TAATGTAAGTGATGACGAGT-----CTATCGCGTCATCGAGTAGTGTGTTTAAATCAAT 5665
Db 5655 UAAUUAUACGUAUGAUGUUGGAGGUCUUGUGCGGAAUCGUAUUGUUAU--AAU 5711
Qy 5666 ATGCTTATACATCAACTCTCCGAGCCAATTTGTTTACTTATCTTCGCTTACGCAGAT 5725
Db 5712 AUGUCUACAGUACACUACUCCAUUCGUGUUGUUGUUGUUGUUGUUGUUGUUGUUG 5771
Qy 5726 CTTGTGACGCTGATCAATCTGTGTACAAATGCTATGGTGAACAGTTTCAAAACGCAACAA 5785
Db 5772 CCAUAGAGUUAUUAUUAUUGUACUAUUGCCUUAAGAAUUAUGUUUUAACAACAACAA 5831
Qy 5786 GCTAGGACAAACAGTCCCAACAGCAATTTGCGGATCGCTGGAAACCTGTGCTTAGTATGACA 5845
Db 5832 GCUCGAACUGUGUUAUUAAGACAAUUCAGUGAGGUGGAAACCTUCCACCAAGUAACU 5891
Qy 5846 GTGAGATTTCTGATCGGATTTCTATGTATAGATATATTCGACGCTTGATCCGTTG 5905
Db 5892 GUUAGUUCUGGACAGUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5951
Qy 5906 ATCAACGCGTTTATTAATAGCTTTGTACTAGAAATAGAAATAGAGGTTGATAATCAA 5965
Db 5952 GUCACAGACUUGUUGGUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6011
Qy 5966 CCGCACCGAATACTACTGAATCGTTAAACGCGACTCAGAGGTAGAGTGTACTGTATA 6025
Db 6012 CGCAACCCACGACUGCGGAAACGUUAGUACUACUGUAGUAGUAGUAGUAGUAGUAG 6071
Qy 6026 GCTATAGGGGTTCAATCAATAATTTGGCTTAATGAATGTTCTGTGGAACCTGGCATGTC 6085
Db 6072 GCCAUAAGGCGCGAUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 6131
Qy 6086 AATCAAGCAGGCTTTGAGACTGTAGTGACTTCTGTGGACCAACTCCGGCTACTTAG 6145
Db 6132 AUUGGAGCUUUCGAGAGCUCUUCUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUG 6191
Qy 6146 CTATT 6150
Db 6192 CAUU 6196

RESULT 8

US-10-828-029-4

; Sequence 4, Application US/10828029

; Publication No. US20040171813A1

GENERAL INFORMATION:

APPLICANT: GARGER, STEPHEN

HOLTZ, R. BARRY

MCCULLOCH, MICHAEL

TURPEN, THOMAS

TITLE OF INVENTION: A PROCESS FOR ISOLATING AND

PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES

FROM PLANT SOURCES

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howrey & Simon

STREET: 1299 Pennsylvania Avenue N.W.

CITY: Washington

STATE: DC

COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/828,029

FILING DATE: 20-Apr-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/962,527

FILING DATE: 24-Sep-2001

APPLICATION NUMBER: 09/037,751

FILING DATE: 10-march-1998

ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P

REGISTRATION NUMBER: 25,277

REFERENCE/DOCKET NUMBER: 00801.0140.999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-463-8109

TELEFAX: 650-463-8400

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 6475 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: Genomic RNA

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-828-029-4

Query Match 38.6%; Score 2452.2; DB 19; Length 6475;

Best Local Similarity 44.8%; Pred. No. 0;

Matches 2770; Conservative 1147; Mismatches 2208; Indels 60; Gaps 8;

Qy 20 ACAACAACAATTAAACAACAAACAACATATTACAACAACAACAACAACAACAATGGCACAC 79

Db 18 ACCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 77

Qy 80 ATCAATCTATATATTAGCAACGCCCTCTTTGAAAGCGTGAGTGGTAAACACCTCTCGTT 139

Db 78 ACACAGACGCUCCACUUCAGCUUUGCUGGACACUUGCCGAGGAAACAACUUCUGUC 137

Qy 140 AATGACCTTCAAGAAGCGCGCATGTACGATACGCCCGTGGAGAAATTTAAACGCCCGCAC 199

Db 138 AUGAUCUACGAAGCGUGCUUUUACGACACACGCGGUUGAAGAGUUUUAACGCGUGAC 197

Qy 200 CGTAGACCAAGGTCAACTTTTCCAAAACCTATTAGCGAAGCAACGCTTCTAGTCTCC 259

Db 198 CGCAGGCCCAAGGUGAACUUUUCAAAAGUAAUAAAGCGAGGACGACGCUUUAUUGUACC 257

Qy 260 AACGCGTACCAGGATTCACAGATTACCTTTTATAATCTCAAAATGCCGTACACAGTTTG 319

Db 258 CGGCGGUUACCAAUUCCAAAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 317

Qy 320 GCTGGAGGTTTGAGAGCATTTAGAAATTTGAAATATCTGATGCTACAAAGTTCCCTATG 379

Db 318 GCAGGUGAUUGCAUCUUAAGAACUGGAAUUAUCUGAUGAUGCAAAUCCUACGGAUCA 377

Qy 380 CCAGCATATCATATAGTGGAACTTTGGACGACATTTGTTTCAAGCAGGAGTATCGTG 439

Db 378 UUGACUUAUGACAUGGCGGAAUUAUUGCAUCUGCUUUAAGGAGCGAGCAUUAUGUA 437

Qy 440 CATTTGCTGATGCTCAATCTGGACATACAGATATATAGGACGAGCAACAAAGGAC 499

Db 438 CACUGCUGCAUGGCCAACCCUGGACUUCUGAGACAUCUUGCGGACAGAGCCAGGAAGAC 497

Qy 500 TCAATTGAGATGTTATTTGTCAGATTGCTCGTTCTTAAACAGGTAAATCTCTGAGTTCAA 559

Db 498 AGUAUUGAACUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 557

Qy	2234	CTATGCAAGTCACTAAAGATGAAGTCGGGTATGATTCTGATTTCCAGGGAGAAAGTTGGT	2299
Db	2238	CUCGUCAAAGAUCCUCRAAGAUACAGCUGCUUUAUGCCUUGAAACCCGUCAAAAGUUGGA	2297
Qy	2294	GTUUGGAGTCTACTTTTGAAAAAGTGCTCCTCAAACTCGCGGCCAAAGTCATTATGCG	2353
Db	2298	GUCUUGAUGUUGUUAUCUAGAAUGUGUUUAUCAAACCAACGGCCAAAGAGUCAGCAUGG	2357
Qy	2354	GGAGTTGTCTCTGGATTACAAAGGGGAAAAATGTTTACTGTGCATCTTCTATCTTTATGAAGGAGAT	2413
Db	2358	GGUUGUUGUAAACCCACGCGAGGAAGUUAUCAUGUGGCGCGCUUUGGAAUAUGAUGAGCAG	2417
Qy	2414	AGAATGTTGACTGAGAGCGACTGGAGAGGGTGGCTGTATCATCTGATCAAAATGGTATAT	2473
Db	2418	GGUGUGUGACAUUGCGAUGAUGGGAAGAGUAGCUGUCAGCUGUGUCUGUUGUUUAU	2477
Qy	2474	TCTGATATTCCAAAGCTCCAAAATCTCAGAGAAACAAATGAGAGACGGTGAACCCACGAA	2533
Db	2478	UCCGCAUUGCGGAAACUCAGAAUCUUGCGCAGACUGUCUGAAACGGAGAAACCGCAUGUC	2537
Qy	2534	CCTACTCAAGAGATGGTACTTTGTGGATGGGGTGCTGGTTGTGGAAGTACAAAGGAGAT	2593
Db	2538	AGUAGCGCAAGGUUGUUCUUGUGGACGGAGUUCGGGCGUGUGGGAAAAACCAAGAAAUU	2597
Qy	2594	TTTGAAAGATTTGATCTTTGATGAGGATTTGATCTTTGGTTCTCTGGAAAAACAAGCTGTGCT	2653
Db	2598	CUUCCAGGGGUAUUAUUUGAUGAAGUACUAUUUAUUGUAGCUGGGAACGAAGCGCGGAA	2657
Qy	2654	ATGATCAGAGAGAGGGCTTAATTCATCTGGACTGATAAGAGCCAAATGGACAATGTGAGA	2713
Db	2658	AUGAUCAGAGACGUGCGAAUUCUUCAGGGAUUAUUGUGGCCACGAAGHACAACGUUAA	2717
Qy	2714	ACGGTAGATTCACTTCTTAATGCAATCCAAAACCGCGATCAC-----ACAAGAGCGCTT	2764
Db	2718	ACCGUUAUUCUUGAUGAAUUAUUUGGAAAGACACACGUCUGUUAUCAAGAGGUUA	2777
Qy	2765	TTTATGATGAAGGGTTGATGCTGCACACCGGTTGTGTTAACTTCTCGTGGTCTTATCTCT	2824
Db	2778	UUAUUGAUGAAGGUGUUGUUGUACUACUGGUGUUAUUUUUUGUGGCGCAUGUCA	2837
Qy	2825	GGTTGCAGCATCGCATACATTTACGGAGATACACAGCAGATTCCTCTTATTAAACAGAGTT	2884
Db	2838	UUGUGCGAAAUUUGCAUUAUGUUUACGGAGACACACAGCAGAUUCCAUACUCAAUAGAUU	2897
Qy	2885	CAGAAATTTCCGGTATCCCAAACATTTTGAGAAGCTGCAAGTGGATGAAGTTGATGATGAGG	2944
Db	2898	UCAGGAUUCGGUACCCCGCCAUUUUGCCAAUUGGAAGUUGACGAGGUGGAGACACGC	2957
Qy	2945	AGGACCACTGATGATGCCAGTGATGTGAAATTTTTTCTTAATCGAAGTACGAAGGA	3004
Db	2958	AGAACTUACUCUCCGUUGCCAGCCCAUGUCAACAUAUUCGAAACAGGAGAUUAGAGGGC	3017
Qy	3005	CGGTTGACACCACTTCAACTGTATACAGTACGGTCTCATCTGAGATGATAGGCGGTAAAG	3064
Db	3018	UUUGUCAUGAGCAUUCUUCGUAUAAAGUCUGUUUCGACGAGAGUUGGCGCGGAGCC	3077
Qy	3065	GGAGTACTAAACAGTGTTCCTCAAAACCACTAAAGGGGAAAATGTTGAACTTTTCACTCAGGCT	3124
Db	3078	GCCGUGAUAUCCGAUCUCUAAAACCCUUGCAUGGCAAGAUCCUGACUUUUAUCCCAUCCG	3137
Qy	3125	GATAAATTTGTAGTAGGAGAGGGCTTATAAGAAATGTGAACAACGGTTTCATGAGATCCAA	3184
Db	3138	GAUAAAGAAAGCUCUGCUUUCAAGAGGGUUAUUCAGAUGUUCACACUGUGCAUGAAGUGCAA	3197
Qy	3185	GGAGAAACCTTTGAAGATGTGTGGTTCAGATTTGACGGCAACTCCACTGACTCTGATT	3244
Db	3198	GGCGAGACAUAUCUCUGAUGUUUACUAGUUAAGGUAUACCCCUACACAGAGUCUCCAUU	3257
Qy	3245	TCCAAGTCTTCCCGCATGTTCTAGTCGCTCTGACTAGACACACAAAGAGCTTCAAAATAT	3304
Db	3258	GCAGGAGACAGCCACAUGUUUUGUGCGCAUUGUACAGGCACACUUGUUGCUCAGAUAUC	3317
Qy	3305	TACACCGTAGTGTAGATCCCTTTTAGTACAGATAAATTAGTGAATTTGTTCTTTAAAGCTCC	3364

[illegible]

Db 4398 AAGAGCGGCGACGUCACGACGUCUUAUUGGAAAACACUCUGUGAUAUUGUCGUAUUGGUC 4457
Qy 4442 TCAATGTGTACCGATGGAAGGTGATATAAGAGTCTTTTGTGAGAGCGATTCGGTTTGT 4501
Db 4458 UCAGUUCUCCGAGGAGAGAAUAUAUUAAGAGGAGCCUUUUGCGGAGAGUAGUCUGUCG 4517
Qy 4502 TATTTTCCAAAGGTTTGGATTTCCCTGACATTCAGTCAATGCTGTAATCTCATGTGGAAT 4561
Db 4518 UACUUCGAAAGGUGUGUGUUCGCGAUGUGCAACUCCGCGAAUUAUUGUGAAU 4577
Qy 4562 TTTGAGGCCAACTGATAGAAAGAGGTACGTTTCTTTGCTAGATACATCATACAC 4621
Db 4578 UUUGAAGCAAAACUGUUUUAUUAACAGUAGGUAUUAUUGCGGAGUAUUAUUAUUAU 4637
Qy 4622 CATGATAGGAGCAATAGTGTATTTATGATCTTTGAAAGTTGATCTCCAAACTTTGGGGCA 4681
Db 4638 CACGACAGAGCAUUGUGUAUUAUGAUCCUUAAGUUAUUGUUAUUGUGUCU 4697
Qy 4682 AAACATATCAAGGATATGATCACTTAGAGAGTTAAGGGTCTTTTGTGGATGTTGCT 4741
Db 4698 AAAACAUCAGGAUUGGGAACACUUGAGAGAGUUCAGAAAGGUCUCUUUGUGAUGUUGCU 4757
Qy 4742 TGTTCGCTCGAAGTCTGTAGGCTTTCCGAGCTGACGAGCTATCAAGAGGTT 4801
Db 4758 GUUUCGUUGAACAAUUGUGGUAUUAUAC---ACACAGUUGAGCAGCGCUGUAUGGAGGUU 4814
Qy 4802 CATAAAACCGGATGATGTTGTTCTGTTTAAATTTGTTTAACTTTTGTGAT 4861
Db 4815 CAUAGAGCCGCCUCCAGGUUCUUUUAUUAAGUUGUGGUAUUAUUGUCUGAU 4874
Qy 4862 AAATTTTATTAAGACTTTTAAATGGCTTTAGTCTCAGAGATCTGCAAAAT 4921
Db 4875 AAAGUUCUUUAAGAGUUAUUAAGUUGGUCUAGUUGUUAUUAAGAAAGGUAUUAU 4934
Qy 4922 TAGCGATTCATGATCTTTGGAACAGGATGATGATCTCCGATCTATGATAGGT 4981
Db 4935 CAUAGAGUUAUACACGUCGACAAUUAUGGAGAAUUAUUAUUAUUAUUAUUAUUAUUAU 4994
Qy 4982 CAAGAGGTGTAGATATCGATGTGGACAAGATTTATGGCTGTTTAAAGATGATGATCTTTC 5041
Db 4995 AAAGAGUUAUUGUUCGAAUUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5054
Qy 5042 TGATGTAGATTTACTTAAGGTGTTAAGTTAGTTAAGAAAGGTTATGTTGCTTAGCTGA 5101
Db 5055 AGAGGUAACCCUUCUUAAGAGUUAUUAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5114
Qy 5102 TTTGCTGATGTCGCGAGTGAATCTCCGATTAACCTCCGCTGCTGCTGCTGCTGCTGCTG 5161
Db 5115 UUUGGUGUCACGCGGAGUGGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5174
Qy 5162 TATTTAGATAGAGAAATGAAAGGAGTGAAGAAAGCAACGCTGGGTGCGTATCAAGCCCC 5221
Db 5175 UCUGUGGACAAAGAGGAAAGAGCGGAGCCACUUCGUAUUAUUAUUAUUAUUAUUAUUAUUA 5234
Qy 5222 TGCTTGCAAAAGAAATTTTCTTTTAAAGTAAATCCCTAAATTAATTAATTAATTAATTAAT 5281
Db 5235 AGUCGCAAGAAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5294
Qy 5282 TGCTGAGAGCAGCCGCGGAGGTTAGTGAATATCAAGAGGAGTGGCTATGGAAGAGG 5341
Db 5295 CGCGAAGAAACGUCGCGGCAAGUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5354
Qy 5342 ATACTGCTTTTATCTTTGAGTTCGTTTCAATTTGTTGATGATACATAAAATAATGTAAG 5401
Db 5355 UUUCUGCGCUUUCUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5414
Qy 5402 AAAAGGTTGAGGAAACGATTTTGTAGTGTGACAGAGGCTCGCGCAATTTGAATCACTGA 5461
Db 5415 AUUAGGUUAGAGAGAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5474
Qy 5462 AAAAGGTTGTCAGAGGTTGCGGATGAGTACCAATGCTGTAACCTCGAAAGGTTTCC 5521
Db 5475 AGAAGUCGUUGAUGAUGUUAUGGAGAAUGUCCUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5534

Qy 5522 GG-----AAAAACAAAAAGAAATGGTAGTAATAATGTTAATAAT----- 5561
Db 5535 AUCUCGAAACCGGAAAAAGAGUGUCCGCAAGGAAAAAUAUAGUAUAUAGUUAUAGUUAUAG 5594
Qy 5562 -----AGAAAAATAAATACAGTGGTAGAGGGTTTTTAAATTTGAGGAAATTTGAGGA 5614
Db 5595 AGUGCCGAACAAGAAUAUAGAAAAUUAAGGAUUUUUGGAGGAUAGAGUUUUAAAAAGAA 5654
Qy 5615 TAAATGAAGTGAAGCAGGT-----CTATCGCGTCAATCGAGTACGTTTAAATCAAT 5665
Db 5655 UAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5711
Qy 5666 ATGCTTTATACAACTCTCCGAGCAATTTGTTTACTTATCTTCCGCTTAGCGAGAT 5725
Db 5712 AUGUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5771
Qy 5726 CTTGTGAGCTGATCAATCTGTGTACAAATGCTTGGGTAAACAGTTTCAAAACGCAACAA 5785
Db 5772 CCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5831
Qy 5786 GCTAGGACAACTGCTCCAAACAGCAATTTGCGGATGCTCGGAACTGTGCTAGTATGACA 5845
Db 5832 GCUCGAACTGUCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5891
Qy 5846 GTGAGATTTCTGATCGGATTTCTATGTGTATAGATATAATTCGAGCTTTGATCCGTTG 5905
Db 5892 GUUAGGUUCCUGACAGUGACUUAUUAAGGUGUACAGGUAUUAUUAUUAUUAUUAUUAUUA 5951
Qy 5906 ATCAGCGGCTTAAATAGCTTTGATCTAGAAATAGATATAATAGAGTTGATTAATCAA 5965
Db 5952 GUCACAGCACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 6011
Qy 5966 CCGCACCGAATCTACTGAAATCGTTAACCGACTCAGAGGCTAGACGATGCTACTGTA 6025
Db 6012 GCGAACCCACGACUGCCGAAACGUUAUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6071
Qy 6026 GCTATAAGGCTTTCAATCAATAATTTGGTAAATGAACTGTTTCTGTTGAACTGGCATGTT 6085
Db 6072 GCCAUAAGGAGCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6131
Qy 6086 AATCAAGCAGGCTTCGAGCTGCTAGGACTGTTGCTGGACCACTCCGCGCTACTTAG 6145
Db 6132 AAUCGAGCUCUUUUGAGAGCUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6191
Qy 6146 CTATTGTTG 6154
Db 6192 CAUUAUUAUG 6200

RESULT 10

US-10-828-029-5

; Sequence 5, Application US/10828029

; Publication No. US20040171813A1

; GENERAL INFORMATION:

; APPLICANT: GARGER, STEPHEN

; HOLTZ, R. BARRY

; MCCULLOCH, MICHAEL

; TURPEN, THOMAS

; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND

; PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES

; FROM PLANT SOURCES

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Howrey & Simon

; STREET: 1299 Pennsylvania Avenue N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

1220	Qy	AGCAAAAGATGACAAAGAGTGTGAGGTCATTTGTTAAATCGTGCATCTTGTTTACACAGTGCCTT	1279
1218	Db	ACUAGUUAAGGACGCGCAAGAGGAGUCUUAUGUGUGUCCAAAGGAUUCUGUGUUUACAGUGCUU	1277
1280	Qy	AATCATATCAGACATATCAAGCCCAAGCGTTAACTTTACCAGAACGTATTATCTTTCCGTG	1339
1278	Db	AACCACAUUCGAACAUACCAAGGCGGAAGCCUUAACAACGCAAAUGUUUUUGUCCUUGUC	1337
1340	Qy	GAGTCTATAAGATCCCGCGTGATAATCAATGCTGTGTACTCTAGGTCCTGAATGGGATGTA	1399
1338	Db	GAUUCGAUUCGAGCGGUUAUCUUAUACGGUUGACACGAGGUCGGAUUGGGAUGUG	1397
1400	Qy	GATAAAGCAATCTTTCAACCCTTGTCTCAATGACTTTCTTTCTTGACAGCTAAAGCTGGCTGCG	1459
1398	Db	GACAAACUUCUUUAACAUCUUGCAUGACGCUUUAUACCGUAUACUAAAGCUUGCGCUU	1457
1460	Qy	CTTCAAGACCATATAGTAATGSGGNAAGTTTCGGTGTCTTGGATTAAGACCCTTCTGGACTT	1519
1458	Db	CUAAGGAUGACUUACUGAUUAGCAAGUUUAUGUCUGGUUCGAAACGGUGGCCAGCAU	1517
1520	Qy	ATTTGGGATGAGGTGGGCAAAATTTTGGGAAAAGTTTTTCCCCACTATCAAGAGAGATTG	1579
1518	Db	GUGUGGAGUAGAUUUCUGCGGCUUUGGGAACGCAUUCUCCUGGUAAGAGAGGCUC	1577
1580	Qy	GTGAGCAGGAAAAATTTCTGATGTAAAGTGAAGATGCTCTGAAGATCAAGATCCCAGATCTG	1639
1578	Db	UUGAACAGGAAAAUUUAUCAGUGGCGAGGCGACGCAUUAAGAGUACAGGUGGCGUGAUCUA	1637
1640	Qy	TATGTCATCTGGAAGACAGGTTTCGTAGCTGAATACACCAAGTCTGAGGAGTTACCGCAT	1699
1638	Db	UAUGUGACCUUCCACGACAGAUUAGUGACUGAGUACAAGGCCUCUGUGGACAUGCCUCG	1697
1700	Qy	CTAGATATCAAGAAGGACTTTAGAAAGAGCTTGAGCAAAATGTACGACGCGGTTTATCAGAATTA	1759
1698	Db	CUUGACAUUAGAAAGAAUGAAAGAAACGGAAGUGAUGUACUAUGCAUUUCAGAGUUA	1757
1760	Qy	TCTATCCTTTAAGGGTGTGTAAATTTTCGATATCCGGAAGTTTCAAAGACATGTGCAAGGCT	1819
1758	Db	UCGGUUAUAGGGAGUCUGACAAAUUCGAUGUUGAUGUUUUUUUCCAGAUUGGCCAAUCU	1817
1820	Qy	TTAGATGTTTAGTCTCTGATGTGGCAGCAGGAGTAAATCGTTGAGTGGCCGAGATAGNAGC	1879
1818	Db	UUGAAAGUUGACCCAAUGACGGCAGCGGAAGGUUAUAGUCGCGGUCAUGACCAUAGAGAC	1877
1880	Qy	GGTTTAACCTCTACTTTTGTATAAGCCCAACCGAGAGAAATGTGGCTAAGGCTCT-----T	1933
1878	Db	GGUCUGACUCUCAUUAUUAAGCAGCAUCUAUGAGCGGAUUGUUGCGCUAGCUUUAACGGAU	1937
1934	Qy	AAAAGCACGGCGTCTGAGGCGGTGGTATGCTTTGAAACCGACATCCGGAAGAGGTGAACGTA	1993
1938	Db	CAAGAGAAGGCUUCAGAGAAGGUGCUUUGUAGUUAUACCUAAGAGAAGUUGAAGAACCUGCC	1997
1994	Qy	AATAAATTTTCTATTCGTGAGAAAGGAGATGTGCTGTGTGTGACAGAAAGTCATGGTTTG	2053
1998	Db	AUGAAGGCUUGCAUGGCGCAGGAGAGUUAACAUUAGCUGGUCUUGCUGAGAUCAUCCG	2057
2054	Qy	ACGAATCTACTTTAGAGCACCGAGGTGTGAGTCCCTCAACGATTTTCCATAAGGCTTGC	2113
2058	Db	GAGUCGCUUUAUUCUUAAGAACGAGAGUAGUGUUUUAAGACAGUUAUUAUUGGCAACG	2117
2114	Qy	GTGGATAGTGTGATTACAAAGCAAAATGGCATCGGTTGTCTACTGCTGCTCACTCAAAGTT	2173
2118	Db	GCAGAUUCGUUAUUCUGUAGACGAUGAGCUUGCAUUGUGUACACGGGUCGGAUUAAGUU	2177
2174	Qy	CAACAAATGAAGAACTATGTGGAACGTTTGGCAGCTTGTGTCCGCCACTGTATCAAT	2233
2178	Db	CAGCAAAUGAAAAACUUUAUCGAUAGCCUGGAGCAUCAUUAUCUGCUGCGGUGUCGAU	2237
2234	Qy	CTATGCAAGTCACTAAAGGATGAAGTCGGGTATCATTTCTGATTCAGGAGAGAAATTTGTT	2293
2238	Db	CUCGUCAGGAUCCUCAAGAUAACGUCUGCUUAUGAACCCUGAACCUGCAAAAGUUGGA	2297
2294	Qy	GTTTGGGATGTCATTTTGA AAAAGTGGCTCTCTCAAACTCGCGGCCAAAGGTCATTTCAATG	2353

Db	2298	GUUUGAUUGUUCUUCAGGAAGUGUUUAUCAAACCGCCAGAGAUUGCAUGG	2357
Qy	2354	GGAGTGTCTCGGTATACAAAGGGGAAAATGTTTACTTGCACTTCTTATCTTATGAAGGAGAT	2413
Db	2358	GGUGUGUUAACCAACCGCAGGAGNAGUAUUAUGUGGCGCUUUGGAAUAUGAUGACGAG	2417
Qy	2414	AGAAATGTGACTGAGAGCGACTGAGAGGGGTGGCTGTATCATCTGATACAAATGGGTATAT	2473
Db	2418	GGUGUGUGACAUUGCGAUGAUGGGAAGAAGUAGCUGCAGCUCUGAGUCUGUUGUUUAU	2477
Qy	2474	TCTGATATTCGAAGCTCCAAATCTGTAGGAAACAATGAGAGACGCTGAACCCACGAA	2533
Db	2478	UCCGACAUUGCGAAACUCAGAAUCUCGCGCAGACUGUCGAAACGGAGAACCGCAUGUC	2537
Qy	2534	CCTACTCCAAAGATGGTACTTGTGGATGGGGTGCCTGGTTGTGGAAAGTACAAAGGAGAT	2593
Db	2538	AGUAGCGCAAGGUUUCUUGUGGACGGAGUUCGCGCUGUGGGGAAACCAAGAAAUU	2597
Qy	2594	TTTGAAAGATTTGATCTTGTATGAGGATTTGATCTTTGGTTCTCTGGAAACAAGCTGCTGCT	2653
Db	2598	CUUUCACAGGGTUAUUUUUGAAGAAGUAUAUUUUUAGUACUCUGGGAAAGCAAGCGCGGAA	2657
Qy	2654	ATGATCAGAAAGGCGCTAATTCATCTGGACTGTATAAGAGCCAAATGGCAATGTGAGA	2713
Db	2658	AUGAUCAGAGAAGUGCGAAUUCUCAGGGAUUAUUGUGGCCAGGAAGHACAACGUUAAA	2717
Qy	2714	ACGGTAGATTCACTTCTTAATGCAT-----CCAAAAACCGCATCACACAAGAGGCTT	2764
Db	2718	ACCGUUAUUCUUCAUGAUAUUUUGGNAAGCACACGUCUGAGUUAUCAAAGAGGUUA	2777
Qy	2765	TTTATGATGAAGGTTGATGCTGCAACACCGGTTGTGTTAACTTCCTGGTGTCTTATCTCT	2824
Db	2778	TUCAUUGAAGGUGUUGAUGUUGCAUACUGUUGUUAUUUUUUGUGGCGAUGUCA	2837
Qy	2825	GGTTGCGACATCGCATACATTTACGGAGATACACAGCAGAGATTCCTTTTATTAAACAGAGTT	2884
Db	2838	UUUGCGAAAUUGCAUAUUGUUUACGGAGACACACAGCAGAUUCCAUAUCAUUAUGAGUU	2897
Qy	2885	CAGAAATTTCCGATTCCTCAACATTTTTGAGAAGCTGCAAGTGGATGAAGTTGAGATGAGG	2944
Db	2898	UCAGGAUUCGGUACCCCGCCAUUUGCCAAUUGGAAGUUGACGAGGUGGACACGCG	2957
Qy	2945	AGGACCACTAGATGCCAGGTGATGTGAAATTTTTTCTTACAACTCGAAGTACGAAGGA	3004
Db	2958	AGAACTUACUCUCGUGUCCAGCGAUGUACACAUAUUCUGAAACAGGAGUAUUGAGGCG	3017
Qy	3005	CGGTTGACACCACTTCAACTGTATACAGATCGTCTCATCTGAGATGATAGCGCGGTAAAG	3064
Db	3018	UUUGUCAUGAGCACUUCUUGCGUUAAAAGUCUGUUUUGCAGGAGAUUGGCGCGGAGCC	3077
Qy	3065	GGAGTACTAAACAGTGTTCCTCAACACTAAAAGGGAAAAATTGTAACTTTTCACTCAGGCT	3124
Db	3078	GCCGUGAUAUCCGAUCUCAAACCCUUGCAUGGCGAAGAUCCUGACUUUUACCAUUG	3137
Qy	3125	GATAAATTTGATTTAGAGGAGAGGGGTATAAGAAATGTGAACACCGTTTCATGAGATCCAA	3184
Db	3138	GAUAAAGAAGCUCUGCUUUAAGAAGGGUAUUCAGAUGUACACUGUGCAUGAAGUGCAA	3197
Qy	3185	GGAGAAACCTTTGAAGATGTGTCTCGTGGTCAGATTTGACGGCAACTCCACTGACTCTGATT	3244
Db	3198	GGCAGAGACAUAUCUCUGAUGUUUCAUAUGUUGUUUAAACCCCUACACCAAGUCUCAUUAU	3257
Qy	3245	TCCAAGTCTTCCCGCATGTTCTTAGTTCGCTCTGACTAGACACACAAAGAGCTTCAAAATAT	3304
Db	3258	GCAGAGACAGCCACAUGUUUUUGUGCAUUGUUCAGGACACACUUGUCCUCAAGUAC	3317
Qy	3305	TACACCGTAGTGTAGATCCTTTTAGTACAGATAAATTAGTGATTGTCTTCTTTAAGCTCC	3364
Db	3318	UACACUGUUGUAUGGAUCCUUUUAUGUAUUAUUAUGAUAUCAUUAUGAUAUCVAGAGAAACU	3377
Qy	3365	TTCTCTTTAGAAATGTATATGGTATAGAACGAGGTAGTAGTACAAATTACAGATGGATGCA	3424

Db 3378 UACUUGUUAUUAUUAAGGUCGUAUGCAGGAAACAUAUAGCAUUAUACAGAUUAGCUUG 3437
Qy 3425 GTGTTCAAAGTCAATAATCTTTTGTGGCAACACCTAAATCAGGAGACTTTCCAGATCTA 3484
Db 3438 GUGUCAAAGGUUCCAAUUCUUUUUGUUGCAGCGCCAAAGACUGGUGAUUAUUCUGAUUG 3497
Qy 3485 CAGTTCTTATTACGATGTATGCTCCCTCGTAAATAGTACTATCTTAACAAGTATGATGCT 3544
Db 3498 CAGUUUAUUAUUAUUAAGUUGUCUCCAGCGCAACAGCACCAUGAUAUUAUUUUGUCU 3557
Qy 3545 GTTACCATGAGGTACCGTGAATAAGTCTTAATGTGAAGATTGTGTTCTTGTATTTTCC 3604
Db 3558 GUUACCAUAGGUUACUGACAUUUAUUAUGAUGUCAAAGUUAUUGCAUUAUUGAUAUGUCU 3617
Qy 3605 AAAAGTATTCCGATCCGCAAGGAGGTGAACCAATGTCTAGAGCCAGTTTTTGCCTACCGC 3664
Db 3618 AAGUCUGUUGCGGCCUUAAGGAUCAAUAUCAAACCAUAUAUCCUAUUGGUACGAACGGCG 3677
Qy 3665 GCGGAACCGCAAGGCTGCAGGACTACTCGAAATCTGTTGCAATGATTAAAGAAAT 3724
Db 3678 GCAGAAUUGCCACGCCAGACUGGACUAUUGGAAAUUUUAGGCGGAUUAUAAAGAAC 3737
Qy 3725 TTCAACGCACAGACTTGCAGGAGCAGATTGACATTCAGAGCACCGCATCTGTTGTAGTA 3784
Db 3738 UUUAAACGACCCGAGUUGUCUGGACUUAUUAUUAUUGAUAUUGAUAUUAUUGUUAUUGUA 3797
Qy 3785 GATAAGTTTTTGTAGTACTTTTATTAATAAAGAAATAATACACAAAAATATTGCTGGA 3844
Db 3798 GAUAAAGUUUUUAUUAUUAUUGCUUUAAGAAAGAAAGAAACCAAAUUAUAAAUUUCU 3857
Qy 3845 GTGATGACGAAGGATTCATGATGATGATGTTGGAACAACAGGAAGTACTATTGGAC 3904
Db 3858 UUGUUCAGUAGAGAGUCUCUCAAUAGAUUGGUUAUAGAAAGCAGGAACAGGUAAUAGGC 3917
Qy 3905 GACTTGGCTACTACAATTTTACAGATCTGCGGCCCATCGATCAGTACAGACATGATC 3964
Db 3918 CAGCUCGCAUUAUUGUUAUUGUUAUUGCCAGCAGUUAUUGAUAUUAUUGAUAUUAUUG 3977
Qy 3965 AAGGCTCAACCAAAACAGAAATTTGACCTTTTCAATTCAGAAATGAAATCCCTGCTCTCAA 4024
Db 3978 AAAGCACAACCAAGCAAAAUUUGGACACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4037
Qy 4025 ACAATGTTCTACCATTCGAAGCAGATCAACGGTATTTTGGCCGGTTTCTCA--GAGCTT 4081
Db 4038 ACGAUUGUGUACCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4097
Qy 4082 ACAAGTTGCTGCTCGAGGCAATTTGATTTCTAAGAAGTTTCTTTTCTTACTAGGAAACT 4141
Db 4098 ACUAGGCNAUUAUUGGACAGUUGUUAUUGGACAGAUUUUUUUUUAUUAUUAUUAUUAUUA 4157
Qy 4142 CCAGAACAGATTCAAGAAATTTTCTCGATCTCGACTCGCAGCTTCTATGATGATGTTA 4201
Db 4158 CCAGCGCAGAUUAGGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4217
Qy 4202 GAATCGGATATTTCTAAGTATGATTAAGTCAAGAACAGATTTTCAATGCTGCTGATGAT 4261
Db 4218 GAGCUGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4277
Qy 4262 GAAATATGGAAGAAATGGGTCTCAATCAGTTTGTGGCCGAAGTGTGGAACAAGGCGAC 4321
Db 4278 GAGAUUUGCGGAUAUUGGUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4337
Qy 4322 AGGAAAAACAATTGGAAGGATTAATTGCTGGAATCAAGACATGCTGTGATGATCAAGG 4381
Db 4338 AGAAAGACCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4397
Qy 4382 AAAAGCGGTGATGCTACTTTTCAATCGGCAATGCTTTAATAGCAGCTTCTGCTGGT 4441
Db 4398 AAGAGCGGGACGUCACGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4457
Qy 4442 TCAATGTTTACCGATGGAAGGTCATAAAGGTCCTTTTGTGGAGACGATTCCTGTTTG 4501
Db 4458 UCGAUGCUUUCGAGGAGAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4517

Qy 4502 TATTTTCCAAAGGTTTGGATTTCCCTGACATTCAGTCACTGTGCTAATCTCATGTGGAAT 4561
Db 4518 UACUUUCCAAAGGUGUGAGUUUCCGGAACAACACUCCGGAUAUUAUUAUUAUUAUUAUUA 4577
Qy 4562 TTTGAGGCCAAATCTGTATAGAAAGAGTACGGTTACTTTTGTGTAGATACATCATACAC 4621
Db 4578 UUUAGAGCAAAACUGUUUUAAAAACAGUAUUGGAUAUUUUUGCGAGAGUAUUAUUAUUAU 4637
Qy 4622 CATGATAAGGAGCAATAGTGTATTATGATCTCTTTGAAGTTGATCTCAAACTTTGGGCA 4681
Db 4638 CACGACAGAGAGUAGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4697
Qy 4682 AAACATATCAAGGATTTATGATCACTTAGAAGATTAAAGGTGCTTTTGTGGATGTTGCT 4741
Db 4698 AAAACAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4757
Qy 4742 TGTTCGCTCGAAACTGGTCTTTAGGCTTTCCGAGCTGAACGAGCATCTCAAGGAGGTT 4801
Db 4758 GUUUUGUU---GAAACAUAUUGUGGUUAUUAACACAGUUGGACGACGCUUAUUGGAGUU 4814
Qy 4802 CATAAAACCGCGATTGATGTTGCTTTTGTGCTTTTAAATTTGTTTAAACAAATTTTGTGTG 4861
Db 4815 CAUAAGACCGCCUCCAGGUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4874
Qy 4862 AAATTTTATTAGAACTTTGTTTTTAAATGCTGTTAGTCTCAGAGATACTGTCAAAAT 4921
Db 4875 AAAGUUUUUUUAGAAUUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4934
Qy 4922 TAGCGAGTTTCATTTGATCTTTTCGAAACAGAGTATGATACTTTCCGCGATTCATGACTAAGT 4981
Db 4935 CAAUGAGUUUAUUGACUGUCAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4994
Qy 4982 CAAGAGTGTAGAAATTCGACTGTGGAACAAGATTATGCTGTTTAAAGAAATGATAGTCTT 5041
Db 4995 AAAGAGUUUAUUGUUCCAAAGUUGAUAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5054
Qy 5042 TGATGTAGATTTACTTAAAGTGTAAAGTGTAGTTAGTTAAGAAAGGTTATGTGCTTAGCTGA 5101
Db 5055 AGAGUGAAACUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5114
Qy 5102 TTTGGTAGTCTCTGGGAGTGAATCTCCGGAATACTCCGCTGCTGCTGCTGCTGCTGCTG 5161
Db 5115 UUGUUCGUCACGCGCGAGUGGAACTUUGCCUGACUAUUAUUAUUAUUAUUAUUAUUAUUA 5174
Qy 5162 TATTGTAGATTAAGAGAAATGAAAGAGTAAAGAGCAACCGCTGGTGGTGGTATCAAGCCCC 5221
Db 5175 UCUGUGGACAAAAGGAUAGAAAGAGCGCGACGAGGCCACUCUCGGAUUAUUAUUAUUAUUA 5234
Qy 5222 TGCTTGCAAAAGAAATTTTCTTTTAACTTAATCCCTTAATTTTCAATAACATCCGAGGA 5281
Db 5235 AGCUGCAAGAAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5294
Qy 5282 TGCTGAGAAGCACCGCTGGCAAGTGTAGTGAATATCAAAAGGAGTGGCTATGGAAGAGG 5341
Db 5295 CGCAUAGAAAAACUCUGGCAAGUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5354
Qy 5342 ATACTGCTCTTATCTTTTGGAGTTCGTTTCAATTTGTTGTTAGTACATAAAAATAATGTAAG 5401
Db 5355 UUUUGUGCCGUUUCUGGAGUUUGUGUGGUGUUUUUAUUAUUAUUAUUAUUAUUAUUAUUA 5414
Qy 5402 AAAAGTTTGGAGGAGTATTTTGTGTCAGACGCGCTCCGCAATTCGAATCACTCACTGA 5461
Db 5415 AUUAGGUUUGAGAGAGAAAGAUUAACAAACGUGAGAGACGGAGGCCCAUGGHACUUUACAGA 5474
Qy 5462 AAAAGTTTGGAGGAGTTCGTTGATGAAGTACCAATCGCTGTGAAACTCGAAAAAGTTTC- 5520
Db 5475 AGAGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5534
Qy 5521 -----CGGAAACAAAAAGAAATTTGTTAGTTAATTTTAAAT----- 5561
Db 5535 AUCUCGAAACCGGAAAAAGAGUGAUGUCCGCAAGGGGAAAAUUAUUAUUAUUAUUAUUAU 5594

Db 198 CGCAGGCCCAAGGTGAACCTTTTCAAAAGTAATAAGCGAGGAGCAGACGCTTATTGCTACC 257
 Qy 260 AACGGGTACCCGGAGTTCCAGATTACCTTTTATAATATCTCAAAATGCGGTACACAGTTTG 319
 Db 258 CGGGCGTATCCAGATTCCAAATTTACATTTTATATACACGCAAAATGCCGTGATTCGCTT 317
 Qy 320 GCTGGAGGTTTGAGAGCAATTAGAATTGGAATATCTGATGCTACAAAGTTCCCTTATGGATGG 379
 Db 318 GCAGGTGGATTCCGATCTTTAGAACTGGAATATCTGATGATGCAAAATCCCTACGGATCA 377
 Qy 380 CGCACATATGATATAGTGGGAACTTTGCAGCACATTTGTTTCAAAGGCGAGGATTAACGTG 439
 Db 378 TTGACTTTATGATAGCGGGAAATTTTGATCGCATCTGTTCAAAGGCGAGCATATGTA 437
 Qy 440 CATTCGTGTATCCCAATCTGCACATACGAGATATAATGAGGACCAAGGACCAAAAGGAC 499
 Db 438 CACTCTGTATCCCAATCTGCACATCTGCAGCATCATGCGGACCAAGGCGCAAGGAC 497
 Qy 500 TCAATTGAGATGATTTGTCAGATTGCTCGTTCTTAAACAAGGTAAATCTCGAGTTTCAA 559
 Db 498 AGTATTGAACTATACCTTTCTAGGCTAGAGAGAGGGGGAAACAGTCCCACTTCCAA 557
 Qy 560 AGGAGGCTTTTAAACAGGTATCGAAGCTCCCAACGAAGTCTGCTCTTAAACTTTT 619
 Db 558 AAGGAAGCATTTGACAGATACGCAAAATTTCTGAAGACGCTGCTGTCCAAATATCTTC 617
 Qy 620 CAGGATTGTCGAATACATCCGCCAGAGATAGTGTGAGAGATACGCTGCTCTGCAAC 679
 Db 618 CAGACAAATGCGCATCAGCCGATGCAAGCAATCAGGCGAGGTGTATGCCATTCGCTACAC 677
 Qy 680 AGTTTGTATGATTAATCTCTGTCATGAGTTTGGAGCTGCGTTAAATATCTTAAAGATATACAT 739
 Db 678 AGCATATATGACATACACCGCATGAGTTCCGGCGGCGCACTCTTGAGGAAATAATGTCAT 737
 Qy 740 GTATGTTATGAGCTTCCATTTTGGCAGAGCAATTAATCTAGACCAAGCGAGGTACG 799
 Db 738 ACGTGTATGCGGCTTCCACTTCTCTGAGAACCTGCTTCTTGAAGATTCATACGTCAT 797
 Qy 800 CTTAATGAATAGGCGCACTTTCAAAGAGAGGTGATGATGTTCTTTTCTTTGCT 859
 Db 798 TTGGACGAATCAACGCGGTTTTTCGCGCGATGGAGACAGTTGACCTTTCTTTTGA 857
 Qy 860 GATGAAAGTACTTTAAATATATAGTCATAAATAACAAATATCTTGCATTTATGATTAATA 919
 Db 858 TCAGAGAGTACTTTAAATTTATGTCATGATTAATCTTAAATTTATGTCGCAAA 917
 Qy 920 TCTTACTTTCTGCTTCTAGTAGAATAGTTTAAAGGAAATTTTATGCTACATGAGGTT 979
 Db 918 ACTTACTTCCGCGCTCTAATAGAGAGGTTTACATGAAGGAGTTTTTATGTCACAGATT 977
 Qy 980 AATACTTGGTTTGTAAATTTACCAAGTAGATACCTATATCTGTACAGAGTGTAGA 1039
 Db 978 AATACCTGTTTGTAAAGTTTTCTAGAAATAGATCTTTCTTTGTACAAAGGTGGCC 1037
 Qy 1040 CAAATAGGCTGTATAGTATCAGTTTCTATGAGGCGATGGAAGACGCTTTGCTTACAAAG 1099
 Db 1038 CATAAAGGTAGATAGTACAGTTTATCTGCAATGGAAGCGCATGGCATTAACAA 1097
 Qy 1100 AAAACCTTGGCATGTTTCAACTGAAAGAGCAATCTTTAGAGACACGCGCTTCGGTTAAC 1159
 Db 1098 AAGACTCTTGGCAATGTGCAACAGCGAGAGATCTCTTTGAGGATTCATCATCAGTCAAT 1157
 Qy 1160 TTTTGGTTCCTTAAGATGAGGACATGTTGATAGTACCGCTGTTGAGGTTCTATTACC 1219
 Db 1158 TACTGTTTCCCAAAATAGGGGATATGGTATGTCATGTTACCATTAATTCGACATTTCTTGGAG 1217
 Qy 1220 AGCAAAAGATGACAAAGGAGTGAAGTCAATGTTTAAATCGTGACTTTCGTTTACAGTGCTT 1279
 Db 1218 ACTAGTTAAGAGCGCGAGGAGTCTTAGTGTCCAAGATTTCTGTGTTTACAGTGCTT 1277
 Qy 1280 AATCATATCAGAACATATCAAGCAAGGTTTAACTTACCAAGACGATTAATCTTTTCGTG 1339
 Db 1278 AACCACATTCGAACATATACAGGCGAAAGCTCTTACATACGCAAAATGTTTTGCTTTGTC 1337

Qy 1340 GAGTCTATAAGATCCCGGTGATATAATCAATGGTGTACTGCTAGTCTGAAATGGGATGTA 1399
 Db 1338 GAATCGATTTCGATCGAGGTAATCATTAACGGTGTGACAGCGAGGTCGAAATGGGATGTG 1397
 Qy 1400 GATAAAGCAATTCCTCAACCCCTTGTCAATGACTTTCTTCTTGCACATTAAGCTGCTGG 1459
 Db 1398 GACAAATCTTTGTTTCAATCTTGTCCATGACGTTTATACCTGTCATTAAGCTTTCGCTT 1457
 Qy 1460 CTTCAAGACGATATAGTAATGGGAAAGTTTCGGTCTGTTGGATAAGACCACTTCTGAACCTT 1519
 Db 1458 CTAAGAGTACTTACTGATTAAGCAAGTTTAGTCTCGGTTTCCGAAACCGTGTGCCAGCAT 1517
 Qy 1520 ATTTGGGATGAGGTGGGCAAAATTTTTCGAAAACGTTTTCCTCCCATATCAAAGAGAGATTG 1579
 Db 1518 GTGCGGATGAGATTTTCGCTGCGCTTTCGGAACGCAATTTCCCTCCGTGAAAGAGAGGCTC 1577
 Qy 1580 GTGACGAGAAAATTTCTGGATGATGATGATGCTCTGAAGATCAAGATCCAGATCTG 1639
 Db 1578 TTGAAACAGGAAATCTTATCAGAGTGGCGGCGACGATTAGAGATCAGGCTGCTGATCTA 1637
 Qy 1640 TATGTACATGGAAGACAGAGTTTCGTAGCTGAATACACCAAGTCTGAGGAGTTTACCGCAT 1699
 Db 1638 TATGTGACTTCCAGCAGAGATTAGTACTGATGATCAAGGCTCTGTGGACATGCTCGG 1697
 Qy 1700 CTAGATATCAAGAAGGACTTAGAAGACTGAGCAAAATGTACGACGCTTATCAGAAATTA 1759
 Db 1698 CTTGACATTTAGGAAGAGATGGAAGAACGGAAGTGTACAAATGCACTTTTACAGAGTTA 1757
 Qy 1760 TCTATCTTAAAGGCTGATTAATTTTCGATATCGGAAGTTTCAAAGACATGTCAGGCT 1819
 Db 1758 TCGGTGTTTAAAGGAGTCTGACAAATTCGATGTTGATGTTTTTCCAGATGTCGAATCT 1817
 Qy 1820 TTAGATGTTAGTCTGATGTGCGACGAGTAATCTGTTGACAGTGGCGGAGAAATGAAGC 1879
 Db 1818 TTGGAAGTTGACCAATGACGCGAGGAGTTTATGTCGCGTCTATGAGCAATGAGAC 1877
 Qy 1880 GGTTTAACTCTTACTTTTGAAGCAACCGAGGAGAAATGTGGCTTAAAGCTCT-----T 1933
 Db 1878 GGTCTGCTCTCACATTTGACGACCTACTGAGGCGAAATGTTGCGCTAGCTTTTACAGGAT 1937
 Qy 1934 AAAACGACGCGCTCTGAGCGCGTGTATGCTTTGAAACCGACATCCGAGAGGTGAACGTA 1993
 Db 1938 CAAAGAGAGGCTTCGAAAGGCTGTTTGGTAGTTTACCTCAAGAGAAAGTTGAAGAACCGTCC 1997
 Qy 1994 AATAAATTTCTTATTTGAGAAAAGGAGATTGCTGCTGTGTGTCAGAAAAGTCAATGTTG 2053
 Db 1998 ATGAAGGTTTCGATGCGCAGAGGAGTTTAAATTTAGTGTGCTTGTCTGGAGATCATCCG 2057
 Qy 2054 ACGAATGTCTAACTTAGAGCACCGAGGTTTGGAGTCCCTCAACGATTTCCATTAAGGCTTGC 2113
 Db 2058 GAGTCTCTTATTTCTAAGAACGAGGAGATAGAGTCTTTTAGACAGATTTTATATGGCAAG 2117
 Qy 2114 GTGGATGATGATTAACAAAGCAATGGATCGGTTGCTACACTGGCTCTACCTCAAGTT 2173
 Db 2118 CGAGATTCGTTTAAATTCGTAAGCAGATGAGTCTGATGTTGTGTACACGCGTCCGATTAAGTT 2177
 Qy 2174 CAAACAAAGCAAACTATGTGACAGTTTGGCAGCTTTCGTTCTCGCCACTGTATCAAAAT 2233
 Db 2178 CAGCAATGAAAACCTTTATCGATAGCTTGGTAGGATCACTATCTGCTCGGTGTCGAT 2237
 Qy 2234 CTATGCAAGTCTCAATAAGGATGAAGTCGGGTTATGATTTCTGATTTCCAGGGAGAAAGTTGT 2293
 Db 2238 CTCGTCAAGATCTTCAAGATACAGTCTGCTATTGACCTTTGAAACCGCTCAAAAGTTTGA 2297
 Qy 2294 GTTTCGGATGTCATTTTGAAGAGTGGCTCTCCAAACCTCGCGGCCAAAGGTCATTCATGG 2353
 Db 2298 GTCTGGATGTTGCTATAGGAAGTGGTTAAATCAAAACCAACCGGCCCAAGGATGATGATGG 2357
 Qy 2354 GAGTTGCTCGGATTAACGGGGAATGTTTACTGCACTTCTATCTTTATGAGGAGAT 2413
 Db 2358 GGTGTTGTTGAAACCCACCGCGAGGAGTATCATGTGGCGCTTTTGGAAATGATGATGACGAG 2417

Qy	2414	AGAAATGCTGACTGAGACGGACTGAGAGGGTGGCTGTATCATCTGTATACAAATGGTATAT	2473
Db	2418	GGTGTGGTGACATCGCATGATTTGGAGAAGAGTAGCTGTAGCTCTGTGTGTTTAT	2477
Qy	2474	TCTGATATTGCAAAAGCTCCAAAATCTCAGGAAACAAATGAGACGGTGAACCCCGAA	2533
Db	2478	TCCGACATGGCGAAACTCAGAACTCTCGCGACACTGCTTCGAAACGGAGAACCGCATGTC	2537
Qy	2534	CCTACTCAAAAGATGGTACTTTGTGGATGGGGTGGCTGTGTGTGAAAGTACAAAGGAGAT	2593
Db	2538	AGTAGCGCAAGGTTGTTCTGTGGACGAGTTCCGGGCTGTGGGAAACCAAGAARATT	2597
Qy	2594	TTTGAAGAATTTGATCTTGATGAGGAATTTGATCTTTGGTTTCTTGAAAAAAGCTGTGCT	2653
Db	2598	CTTTCCAGGGTTAATTTTGTAGAAAGATCTAATTTTAGTACCTGTGGAAAGCAAGCGCGGAA	2657
Qy	2654	ATGATCAGAAAGGGCTAATCTCATCTGGACTGATAGAGCCCAATGGACAAATGTCAGA	2713
Db	2658	ATGATCAGAAAGCGTGGAAATTCCTCAGGGATTAATGTGGCCACGAAGGACAAAGTTAAA	2717
Qy	2714	ACGGTAGATTCACTTTCAATGTCAT-----CCAAAAACCGCGATCACACAAGAGGCTT	2764
Db	2718	ACCGTTGATTCTTTTCATGATGAATTTTGGGAAAGCACACGCTGTCAAGTTCAAGAGTTA	2777
Qy	2765	TTTATTGATGAAGGGTTGATGCTGCACACCGGTTGTGTTAACTTCTCTGGTGTCTTATCTCT	2824
Db	2778	TTCAATTGATGAAGGGTTGATGTTGCATACCTGTTGTGTTAAATTTTCTTGTGGCGATGTCA	2837
Qy	2825	GGTTGGCAGATCGCATACATTTACGGAGATACACAGCAGATTCCTTTTCATTTAAACAGAGTT	2884
Db	2838	TTGTGGCAAAATGCTATGTTTACGGAGACACACAGCAGATTCCTATCATCATATAGAGTT	2897
Qy	2885	CAGAAATTTCCCGTATCCAAACATTTTGAGAAGCTGCAAGTGGATGAAGTTGATGAGG	2944
Db	2898	TCAGGATTTCCGTATCCCGCCCAATTTTGCCAAATTTGGAAGTTGACGAGGTGGAGACACGC	2957
Qy	2945	AGGACCACTGAGATGCGCAGGTGATGTGAATTTTTCCTACAATCGAAGTACGAAGGA	3004
Db	2958	AGAACTACTCTCCGTTGTCCAGCGCATGTCCACAATTTCTGAAACAGGAGATATGAGGCG	3017
Qy	3005	GCGGTGACAAACCTCTCAACTGTACACGATCGGCTCATCTGAGATGATAGGGGGTAAG	3064
Db	3018	TTTGTGATGACCACTTCTCGGTTAAAGTCTGTTTCGAGGAGATGGTCGGCGGAGCC	3077
Qy	3065	GGAGTACTAAACAGTGTTCAAAACCACTAAAGGGGAAAATTTGAATTTTCACTCAGGCT	3124
Db	3078	GCCGTGATCAATCCGATCTCAAAACCCCTTGATGGCAAGATCCCTGACTTTTACCCAATCG	3137
Qy	3125	GATAAATTTGATTAGGAGAGGGCTATAGAAATGTGAACACCGTTTCATGAGATCCAA	3184
Db	3138	GATAAAGAAGCTCTGCTTTCAAGAGGGTATTTCAAGATGTTCACTGTGCAATGAAGTGCAA	3197
Qy	3185	GGAGAAACCTTTGAAGATGTGCTGCTGTGATGATGCGGCAATCCCACTGACTCTGATT	3244
Db	3198	GGCGAGACATACTCTGATGTTTCACTAGTTAGTTTAAACCCCTACACCACTCCCATCTT	3257
Qy	3245	TCCAAGTCTTCCCGCATGTTCTAGTCGCTCTGACTAGACACAAAGAGCTTCAAAATAT	3304
Db	3258	GCAGGAGACGCCACATGTTTGGTCGATTTGTCAAGGCACACCTGTGCTCAAGTAC	3317
Qy	3305	TACACCGTAGTTGTAGATCCCTTTTAGTACAGATAATTAGTGAATTTGTCTTTTAAGCTCC	3364
Db	3318	TACACTGTTGTATGGATCCCTTTAGTTAGTATCATTTAGAGATCTAGAGAACTTTAGCTCG	3377
Qy	3365	TTCTCTTTTGAAGAAATGATATGTTAGAACGAGGTAGTAGCAATTTACAGATGGATGCA	3424
Db	3378	TACTTGTTAGATATGATTAAGGTGATGCAGGAACACAAATAGCAATTTACAGATTTGACTCG	3437
Qy	3425	GTGTTCAAAGTCAATAATCTCTTTGTGGCAACACTAAATCAGGAGACTTTTCCAGATCTA	3484
Db	3438	GTGTTCAAAGGTTCCAAATCTTTTGTGCGAGCGCAAGACTGTGGATATTTCTTGATATG	3497
Qy	3485	CAGTTCTATTACGATGATGCTCCCTGGTAAATAGTACTATACTTTAAACAAGTATGATGCT	3544

Db	3498	CAGTTTACTATGATAGTGTCTCCAGGCGACAGACCATGATGAATAATTTTGTATGCT	3557
Qy	3545	GTTTACCATTGAGGTTACGTTGATAATAGTCTTAAATGTGAAGGATTTGTCTTTGATTTTCC	3604
Db	3558	GTTTACCATTGAGGTTGACTGACATTTTCATTGAATGTCAAAGATTGCATATTTGGATATGCT	3617
Qy	3605	AAAAGTATTTCCGATGCGCAAGGAGGTGAACCAATGTCTAGAGCCAGTTTTCGCTACCGCG	3664
Db	3618	AAGTCTGTGCTGCGCTAAGGATCAAAATCAAAACCACTAATCTATGTTGGTACGAACGCGC	3677
Qy	3665	GCGGAACCGCAAGGGCTCGAGCACTCTCGAAAATCTGGTTGCAATGATTTAAAGAAAT	3724
Db	3678	GCAGAAATGCCAGCCAGACTGGACTATTGGAATAATTTAGTGGCGATGATTTAAAGGAAC	3737
Qy	3725	TTCAACGCACACAGACCTGACGGGACGATTCACATTTGAGAGCACCGCATCTGTTGTAGTA	3784
Db	3738	TTTAAACGACCCGAGTTGTCTGCAATCATTTGATATTGAATAATCTGCACTTTTAGTTGTA	3797
Qy	3785	GATAAGTTTGTGATAGCTAATTTTATAAAAAAGAAAATACACAAAATAATTTGCTGGGA	3844
Db	3798	GATAAGTTTGTGATAGTTATTTGCTTTAAAGAAAAAGAAAACCAATAAAAAATGTTTCT	3857
Qy	3845	GTGATGACGAAGATTCAATGATGAGATGGTTGGAACACAGGAAGAAAGTACTATTTCGAC	3904
Db	3858	TTGTTCAGTAGAGAGTCTCTCAATAGATGGTTAGAAAGCAGGAACAGGTAACANTAGGC	3917
Qy	3905	GACTTGGCTAACTACAAATTTTACAGATCTCCGCGCCATCGATCAGTACAGACACATGATC	3964
Db	3918	CAGCTCGCAGATTTTGAATTTTGTAGATTTGCCAGCAGTTGATCAGTACAGACACATGATT	3977
Qy	3965	AAGCTCAACCAAAAACAGAAATTTGGACCTTTTCAATTTAGAAATGAATACCTGCTCTGCAA	4024
Db	3978	AAAGCACAAACCAAGCAAAAATTTGGACACTTCAATCCAAAACGGAGTACCCGCGCTTGCAG	4037
Qy	4025	ACAATTTCTCTACCACTCGAAGCAGATCAACGGTATTTTGGCCGGTTTCT--CAGAGCTT	4081
Db	4038	ACGATTTGTGTACCATTCAAAAAAGATCAATGCAATATTTGGCCGTTGTTTAGTGAGCTT	4097
Qy	4082	ACAAGGTTGCTGCTCGAGGCAATTTGATTTCTAAGAAGTTTCTTTTCTTACTAGAAAAC	4141
Db	4098	ACTAGGCAATTTACTGGACAGTGTGATTTGAGCAGATTTTGTGTTTTCACAAGAAAGACA	4157
Qy	4142	CGAGAACAGATTCAGAAATTTTCTCGGATCTCGACTCGACAGTTCTCTATGGATGTGTTA	4201
Db	4158	CCAGCGCAGATTGAGGATTTCTTCCGAGATCTCGACAGTCACTGTGCCGATGGATGTCTTG	4217
Qy	4202	GAACTGGATATTTCTAAGTATGATAGTCAAGAACGAGTTTCAATGCTGTGTAGAGTAT	4261
Db	4218	GAGCTGGATATATCAAAATACGAATACTCAGAAATGAAATTCCTGTGCGATGAGATAC	4277
Qy	4262	GAAATATGAAAAAGATTTGGGTCTCAATGAGTTTTCGCGCAAGTGTGGAACAAAGGCGAC	4321
Db	4278	GAGATCTGGCGAAGATTGGGTTTGAAGACTTCTTGGGAGAGTTTGGAAACAAAGGCGAT	4337
Qy	4322	AGGAAACAACTTTGAAGGATTAATTTGCTGGATCAAGACATGCTGTGGTATCAAGG	4381
Db	4338	AGAAAGACCACTTCAAGGATTTATACCGCAGGTATAAAAACTTGCATCTGGTATCAAGA	4397
Qy	4382	AAAAGCGGTGATGTGACTACTTTTCATCGCAATACTGTTATAATAGCAGCTTGTCTGGGT	4441
Db	4398	AAGGCGGGAGCTCAGCAGCTTCATTGGAACAACTGTGATCATTTGTCATGTTTGCC	4457
Qy	4442	TCAATGTTTACCGATGGAAAAAGTCAATAAAAGGTGCTTTTTTGTGGAGACGATTCGTTTTG	4501
Db	4458	TCGATGCTTCCGATGGAGAAAAATAACAAAGGAGCCCTTTTGGCGTGACGATGCTGCTG	4517
Qy	4502	TATTTTCCAAAGGTTTGGATTTCCCTGACATTTCACTGATGCTGCTAATCTCATGTGGAAT	4561
Db	4518	TACTTTCCAAAGGTTGTGAGTTTCCGGATTTCCGCAACACTCCCGGAAATCTTATGTGGAA	4577
Qy	4562	TTTGAGGCCAAACTGTATAGAAAGAGGTACGGTTTACTTTTTTGTGTAGATACATACAC	4621

```

Db 4578 TTTGAAGCAAACTGTTTAAACCAACAGTATGATATCTTTTGGGAAGATATGTAAATACAT 4637
Qy 4622 CATGATAAGGAGCAATAGTGTATATGATCTCTTTGAAGTTGATCTCCAAACTCTGGGCA 4681
Db 4638 CACGACAGAGATGATGTGTATATGATATCCCTTAAGTTGATCTCCAACTTGGTGT 4697
Qy 4682 AAACATATCAAGGATATGATCACTTGAAGAGTTTAAAGGTTCTTTTGGGATTTGCT 4741
Db 4698 AAACACATCAAGGATTTGGGAACACTTGGAGAGTTTCAAGAGTCTCTTTGTGATTTGCT 4757
Qy 4742 TGTTCGCTCGGAACTGTTGCTTGAAGCTTTCGCGAGCTGAAGCAGCTATCAAGAGTT 4801
Db 4758 GTTTCGTT---GAACAATTTGTCGCTATTACACACAGTTTGGAGCGCTGTATGGAGTT 4814
Qy 4802 CATAAACCGGATGATGTTGCTGTTTAAATTTGTTTAAACAAATTTTGTGTGAT 4861
Db 4815 CATAGACCGCCCTCCAGGTTTCTTTTAAAGTCTGGTGTGATTTTGTCTGAT 4874
Qy 4862 AAATTTTATTTAGAACTTTGTTTAAATGGCTGTAGTCTTCAGAGATATCTGCAAAAT 4921
Db 4875 AAAGTTCTTTTGAAGTTTGTATATAGTGTCTAGTTTGAAGGAAAGTGAATAT 4934
Qy 4922 TAGCGAGTTCAATGATCTTTGCAACACAGATGAGATATCTCCGGCAATCATGACTAAGT 4981
Db 4935 CAATCAGTTTATCGACCTGACAAAATGGAGAAGATCTTACCGTCGATGTTTACCCCTGT 4994
Qy 4982 CAAGAGTGTAGAAATATGACTGTGCAAGATATGCTGTTAAGAAATGATAGTCTTTC 5041
Db 4995 AAAGAGTGTATGTTGTTCAAGTTGATATAAATATGTTTCAAGAAATGATGCTTTC 5054
Qy 5042 TGATGTAGATTTACTTTAAAGTGTAAAGTTAGTTTAAAGAGGATGTGTGCTTAGCTGA 5101
Db 5055 AGAGTGAACCTTCTTAAAGGAGTTAAGCTTATGATAGTGAATGCTGTTTGAACCG 5114
Qy 5102 TTTGTAGTGTCTGGGAGTGAATCTCCCGATTAATCTCCGCTGGTGTGCTGAGTGTG 5161
Db 5115 TTTGTCGTCTACGGCGAGTGGAACTTGCCTGACAAATTCGAGAGAGTGTGAGCGTGTG 5174
Qy 5162 TATTGTAGTATAGAAATGAAAGAGTAAAGAGTAAAGCAACGCTGGTGTGCTATCACGCC 5221
Db 5175 TCTGTGGCAAAAGGATGGAAGAGCCGACGAGGCCACTCTCGGATCTTACTACACAGC 5234
Qy 5222 TGCTTGCACAAAGAAATTTTCTTTTAAAGCTAATCCCTAATTTCAATAACATTCGAGGA 5281
Db 5235 AGCTGCAAGAAAGAAATTTCAAGTCTAGTCTAGTCTGTTCCCAATTTATGCTATAACCCAGGA 5294
Qy 5282 TCTCAGAAAGCAGCCGTCGAAAGTGTAGTGAATATCAAGAGTGGCTATGGAAGAGG 5341
Db 5295 CGCGATGAAACGCTGCGCAAGTTTGTAGTAAATTTAGAAATGTGAAGATGTGACGCGG 5354
Qy 5342 ATACTGTCCTTTATCTTTGGAGTTCGTTTCAATTTGTGTAGTACATATAAATAATCTAAG 5401
Db 5355 TTTCTGTCGCTTCTCTGGAGTTTGTGTCGCTGTGTATTTGTATAGAAATAATATAAA 5414
Qy 5402 AAAAGTTTGGGGAACGTTATTTTGTAGTGTGACAGACGCTCGCCAAATTTGAATCACTGA 5461
Db 5415 ATTAGTTTGGAGAGAAATTTACAAAGTGTGAGACGAGGCGCCATGGAATCTACAGA 5474
Qy 5462 AAAGGTTTGTGAGGAGTTCGTTGATGAAGTACCAATGGCTGTGAACTCGAAAGGTTTC 5520
Db 5475 AGAAGTCTGTTGATGAGTTTCAATGGAAGATGTCCCTATGTGATCAGGCTTGCAGAGTTTC 5533

```

RESULT 14

```

US-09-993-059-33
; Sequence 33, Application US/09993059
; Publication No. US2002008024A1
; GENERAL INFORMATION:
; APPLICANT: GARGER, Stephen A.
; APPLICANT: TURPEN, Thomas H.
; APPLICANT: KUMAGAI, Monto H.
; TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
; TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION

```

```

; FILE REFERENCE: 008010087CPUS06
; CURRENT APPLICATION NUMBER: US/09/993,059
; CURRENT FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 11641
; TYPE: DNA
; ORGANISM: Tobacco mosaic virus
US-09-993-059-33

```

```

Query Match 36.1%; Score 2291.4; DB 9; Length 11641;
Best Local Similarity 64.0%; Pred. No. 0;
Matches 3532; Conservative 0; Mismatches 1966; Indels 21; Gaps 4;

```

```

Qy 20 ACAACAACTTAAACCAAAACAAACATATTACAAACAAACAAACAAACAAACAAACAAAC 79
Db 18 ACCAACACAAACAAACAAACAAACATTAACATTTACTATTATTACAAATACAAATGCAAT 77
Qy 80 ATACAATCTATAATTAGCAACGCCCTTCTTGAAGCGTGAAGTGTGTAAGAAACAACTCTGTT 139
Db 78 ACACAGACAGCTACCAATCAGCTTTGCTGGACACTGTCCGAGGAAACAACTCTCTGGTC 137
Qy 140 AATGACCTTGAAGAGGCGCATGTACGATACGCGCGTGAAGAAATTTAAACGCCCGCAC 199
Db 138 AATGATCTAGCAAGCGCTGCTTTTACGACACAGCGGTTGAAGAGTTTAAACGCTCGTGAC 197
Qy 200 CGTAGCAAAAGGTCAACTTTTCCAAACTATTAGCGAAGAGCAAAACGCTTCTAGTCTCC 259
Db 198 CGAGGCCAAGGTGCACTTTTCAAAAGTAATAGCGAGGAGCAGACGCTTATTGCTACC 257
Qy 260 AACCGTACCCGAGTTCAGATTAACCTTTTATAATATCTCAAAATGCCGTAACAGTTTG 319
Db 258 CGGCGGTATCAGAAATCCAAATTAACAATTAACAGCAAAATGCCGTCATTCGCTT 317
Qy 320 GCTGAGGTTTGAGAGCAATTAAGATTTGGAATATCTGATGCTACAGTTCCCTATGATCG 379
Db 318 GCAGGTGATTTGCGATCTTTAGAACTGGAATATCTGATGATGCAAAATCCCTACCGATCA 377
Qy 380 CCGACATATGATATAGTGGGAACCTTTCAGACACATTTTGTTCAAAGGCGAGGATTAACG 439
Db 378 TTGACTTTATGACATAGCGGGAATTTTGCATCGATCTGTTCAAGGACGAGCATATGTA 437
Qy 440 CATTCCTGTATGCCCAATCTGGACATACGAGATATAATAGAGCAAGAGCAAAAGGAC 499
Db 438 CACTCTGTATGCCCAACCTGACGCTTCGAGACATCATCGCGCACGAAGGCCAGAAAGAC 497
Qy 500 TCAATTGAGATGTTTGTCCAGATTTGCTGTTCTAACAAGTAAATCTCTGAGTTTCAA 559
Db 498 AGTATTGAATATATCTTTCTAGGCTAGAGAGAGGGGGAACAGTCCCACTTCCAA 557
Qy 560 AGGAGGCTTTTAAACAGGTATGCAAGAGCTCCCAACGAAGTCTGCTGCTTAAACCTTTT 619
Db 558 AAGGAAGCATTTGACAGATACGCAAAATTTCTGAAAGCGCTGTCTGTCAATATCTTTC 617
Qy 620 CAGGATTTGCAATATACATCCGCCAGAGAAATAGTGTGTAAGAGATACGCTGTGCTGCA 679
Db 618 CAGACAAATCGGACATCAGCCGATGAGCAATCAGGACAGTGTATGCCATTTGCGCTACAC 677
Qy 680 AGTTGTATGATATTTCTGTGTCATGAGTTTGGAGTGTGCTTAAATATCTAAGAAATATACAT 739
Db 678 AGCATATATGACATACCAAGCGGATGAGTTTCGCGGCGGCACTCTTGAGGAAAAATGTCCAT 737
Qy 740 GTATGTATGACAGTCCCAATTTTGGCAGAGCATTTACTAGACAGAGGTTTACG 799
Db 738 AGTGCTATGCGGCTTTCCACTTCTCTGAGAACTGCTTCTTGAAGATTCATACGCAAT 797
Qy 800 CTTAATGAAATAGGCGCAACTTTCAAAAGAGAGGATGATGATGTTTCTTTTCTTTGCT 859
Db 798 TTGAGCAAAATCAACGCGGTGTTTTTCGCGCGATGGAGCAAGTGTGACCTTTCTTTTGA 857
Qy 860 GATGAAAGTACTTTAAATATATAGTGCATATAAATAACAAATATCTTGCATTTAGTTAA 919
Db 857 GATGAAAGTACTTTAAATATATAGTGCATATAAATAACAAATATCTTGCATTTAGTTAA 919

```

Db 858 TCAGAGAGTACTCTTAATATTGTGCATAGTTATTCTAAATATTCTTAAGTATGTGCAAA 917
Qy 920 TCTTACTTTCTGCTTCTAGTAGAATAGTTTACTTTTAAAGGAATTTTTPAGTCACTAGGGTT 979
Db 918 ACTTACTTCCGGCTCTATAGAGAGGTTTACATGAAGAGGTTTATAGTCACCAAGGTT 977
Qy 980 AATACTTGGTTTGTAAATTTACAAAGTAGATACCTATATTCTGTACAAAGAGTGTAGA 1039
Db 978 AATACCTGGTTTGTAAAGTTTCTAGAAATAGATACTTTTCTTTTGTACAAAGGTTGGCC 1037
Qy 1040 CAAGTAGGGTGTAGTAGTACAGTCTATGAGCGGATGGAAGCGCTTTGTCTTACAAG 1099
Db 1038 CATAAAAGTGTAGTAGTACAGGAGTTTATCTGCAATGGAAGCGCATGGCAATTACAA 1097
Qy 1100 AAAACCTTGGCCATGTTCAACACTGAAAGGCAATCTTTTAGAGACACGGCTTCGGTTAAC 1159
Db 1098 AAGACTCTTGCAATGTGCAACAGCGAGAGAATCCTCTTGAGGATTCATCATCAGTCAAT 1157
Qy 1160 TTTTGGTTCCCTAAGATGAAGGACATGGTGTAGTAGTACCGTGTGTAGGGTTCTATTACC 1219
Db 1158 TACTGGTTTCCCAAAATGAGGGATATGGTCAATCGTATACCATTTATTTCGACATTTCTTTGGAG 1217
Qy 1220 AGCAAAAGATGACAAAGAGTGAAGTCAATGTTTAAATCGTGAATTCGTTTACACAGTGCCT 1279
Db 1218 ACTAGTAAGAGGACCGCAAGGAAGTCTTAGTGTCCAAGGATTTCTGTTTACAGTGCCT 1277
Qy 1280 AATCATATCAGAAATATCAAGCCAAAGCGTTAACTTTACCAGAAACGTAATTATCTTTCTGTG 1339
Db 1278 AACCACATTCGAATCCAGGCGAAGCTCTTATACATACGCAATGTTTGTCTCTTGTGTC 1337
Qy 1340 GAGTCTATAGATCCCGGTGTGATAATCAATGGTGTACTGCTAGGTCTGAATGGGATGTA 1399
Db 1338 GAATCGAATTCGATCGAGGGTAATCATTAACGGTGTGACAGCGAGGTCGGAATGGGATGTG 1397
Qy 1400 GATAAGCAATCTTCAACCTCTGCAATGACTTTCTTTGACAGACTAAGCTGGCTGCG 1459
Db 1398 GACAAATCTTTGTTTACAAATCTCTGTCCATGACGTTTACCTGCAATCTAAGCTTTGCCGTT 1457
Qy 1460 CTTCAAGACGATATAGTAATGGGAAAGTTTCGGTGTCTTGGATAAGACCACTTCTGAACCT 1519
Db 1458 CTAAGGATGACTTACTGATTAGCAAGTTTAGTCTCGTTTGGAAACGGTGTGCCAGAT 1517
Qy 1520 ATTTGGGATGAGGTGGGCAAAATTTTGGAAACGTTTCCCACTATCAAGAGAGATTG 1579
Db 1518 GTGTGGGATGAGATTCCTGCTGGCGTTTGGGAACGCAATTTCCCTCCGTGAAAGAGAGCTC 1577
Qy 1580 GTGAGCAGGAAAATCTTGGATGTAAGTGAGAACTCTCTGAAGATCAAGATCCCAAGACTG 1639
Db 1578 TTGAAACAGGAAACTTATCAGAGTGGCAGGCGACGCAATTAGAGATCAGGGTGCCTGATCTA 1637
Qy 1640 TATGTCAATGGAAGAAGCAGGTTCCGTAGCTGAATACACCAAGTCTGAGGAGTTACCGCAT 1699
Db 1638 TATGTGACCTTCCACGACAGATTAGTGACTGAGTACAAGGCTCTGTGGACATGCCCTGCG 1697
Qy 1700 CTAGATATCAAGAAGGACTTAGAAGAGCTGAGCAATGTACGACGCGTTATCAGAATTA 1759
Db 1698 CTTGACATTAGAAGAAGATGGAAGAAACGGAAGTGTATCAATGCACTTTACAGAGTTA 1757
Qy 1760 TCTATCTTAAAGGTGCTGATAATTTTCGATATCGGAAGTTTCAAGACATGTGCAAGGCT 1819
Db 1758 TCGGTGTTAAGGGAGTCTGACAAATTCGATGTTGATGTTTTCGCCAGATGTGCCAATCT 1817
Qy 1820 TTAGATGTTAGTCTGTAGTGGCAGCACGAGTAATCTGTGAGTGGCGCGGAATATAGAAGC 1879
Db 1818 TTGGAAGTTGACCCAAATGACGCGACGGAAGGTTATAGTCCGGTTCATGAGCAATGAGAGC 1877
Qy 1880 GGTTTAACTCTTACTTTTGTAAAGCAACCGAGAGATGTGGCTTAAGGCTCT-----T 1933
Db 1878 GGTCTGACTCTCACAATTTGAAACGACCTACTGAGCGGAATGTGTGCGTACTAGCTTTACAGGAT 1937
Qy 1934 AAAAGCAGCGGCTCTGAGGCGGTGTGTGCTTGAACCGACATCCGAAGAGGTTGAACGTA 1993
Db 1938 CAAGAGAAGGCTTCAGAAAGGTGCTTTGGTAGTTTACCTCAAGAGAAGTTGAAGAACCGTCC 1997

Qy 1994 AATAAATTTTCTATTGCTGAGAAAAGGAGATTCCTGCTGTGTGTGTCAGAAAGTCACTGGTTG 2053
Db 1998 ATCAAGGGTTCGATGGCCAGAGGAGAGTTTAAATATTAGTCTGTCTTGTCTGGAGATCATCCG 2057
Qy 2054 ACCAATCTTAACCTTAGAGCACACGAGGAGTTGAGGTCCTCAACGATTTTCCATAAGGCTTGC 2113
Db 2058 GAGTCGTCTTATTCTAAGAACGAGGAGATAGAGTCTTTTAGAGCAGTTTTCATATGGCAACG 2117
Qy 2114 GTGGATAGTGTGATTAACAAAGCAAAATGGCATCGGTTGTCTTACACTTGGCTCACTCAAAAGTT 2173
Db 2118 GCAGATTCGTTAATTCGTAAGCAGATGAGCTCGATGTGTGTACACGGGTCCGATTTAAAGTT 2177
Qy 2174 CAACAAATGAAGAACTATGTGGACAGTTTGGAGCTTCTGTTGCCACACTGTATCAAT 2233
Db 2178 CAGCAAAATGAAAACTTTATCGATAGCTTGGTAGCATCACTATCTGCTGCGGTGTGCAAT 2237
Qy 2234 CTATGCAAGTCACTAAAGGATGAAGTCGGGTATGATTCTGATTTCCAGGGAGAAAGTTTGGT 2293
Db 2238 CTCGTCAAGATCTCTCAAGATACAGCTGCTTATTGAACCTTGAAACCCGTCAAAAGTTTGGGA 2297
Qy 2294 GTTTGGGATCTCACTTTTGA AAAAGTGGCTCCTCAAAACCTCGCGCAAAAGGTCATTCAATGG 2353
Db 2298 GTCTGGAGTGTCACTAGCACTAGGAAGTGGTTAATCAAAACCAACGCGCAAGAGTCAATGCATGG 2357
Qy 2354 GGAGTTGTCTCGGATTAACAAAGGGGAAAATGTTTTACTGCACTTCTATCTTATGAAGGAGAT 2413
Db 2358 GGTGTTGTTGAAAACCCACGCGAGGAAGTATCATGTGGCGCTTTTGGAAATATGATGAGCAG 2417
Qy 2414 AGAATGGTGAATGAGAGGACTCGAGGAGGCTGGCTGTATCATCTGTATACAATGGTATAT 2473
Db 2418 GGTGTGGTGAATGCGGATGATTGGAGAAAGTAGTGTCTGAGCTCTGAGTCTGTTGTTTAT 2477
Qy 2474 TCTGATATTCCAAAGCTCCAAAATCTGAGGAAAAACAAATGAGAGACGCTGAAACCCACGAA 2533
Db 2478 TCCGACATGCGGAAACTCAGAACTCTGCGCAGACTGCTTCGAAACGAGAAACCGCATGTC 2537
Qy 2534 CTTACTGCAAAAGATGGTACTTGTGGATGGGGTCTGGTTGTGGAAAGTACAAGGAGAT 2593
Db 2538 AGTAGCGCAAAAGGTGTTCTTGTGGACGAGTGTCCGGGCTGTGGGAAAAACCAAAAGAAAT 2597
Qy 2594 TTTGAAAGATTTGATCTTGATGAGGATTTTGTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTCT 2653
Db 2598 CTTTCCAGGGTTAATTTTGAAGAGATCTAATTTTGTAGTACTTGGAAAGCAAGCCCGGAA 2657
Qy 2654 ATGATCAGAAAGAGGGCTAATCTGGAATGATAGAGCCCAATTTGGAACAATGTGAGA 2713
Db 2658 ATGATCAGAAAGACGTGCGAATTCCTCAGGGATTTATTGTGGCCACGAAGGACAACGTTAAA 2717
Qy 2714 ACGGTAGATTCACCTTCTAATGCAAT-----CCAAAACGGCGATCACACAGAGGCTT 2764
Db 2718 ACCGTTGATTTCTTTCATGATGAATTTTGGGAAAAAGCACAGCTGTCTGATTTCAAGAGGTTA 2777
Qy 2765 TTTTATGATCAAGGGTTGATGTGCACACCGTTTGTGTAACTTCTCTGTTGCTTATCTCT 2824
Db 2778 TTAATGATGAAGGGTTGATGTGCATACCTGTTGTTGTTAATTTTCTTGTGGCGATGTCA 2837
Qy 2825 GGTTCGACATCGCATACATTTTACGGGATACACAGCAGATTTCTTTTCAATTAACAGAGTT 2884
Db 2838 TTGTGCGAATTCGATATGTTTACGGAGACACACAGCAGATTTCCATACATCAATAGAGTT 2897
Qy 2885 CAGAAATTTCCCGTATCCCAAAACATTTTGAAGCTGCAAGTGGATGAAGTTGAGATGAGG 2944
Db 2898 TCAGGATTTCCCGTACCCCGCCCAATTTTGGCAAAATGGAAAGTTGACGAGGTGGAGACACGC 2957
Qy 2945 AGGACCACTGAGATCCCGAGGTGATGTCAAATTTTTTCTTCAATCGAAGTACGAAGGA 3004
Db 2958 AGAACTACTCTCCGTTGTCCGCGATGTCAACATTTATCTGAACAGAGATATGAGGCG 3017
Qy 3005 GCGGTGACAAACCACTTCAACTGTACAACGATCGGTCTCATCTGTAGATGTATAGCGGTAAAG 3064
Db 3018 TTTGTGATGACACTTCTTCGGTTTAAAAAGTCTGTTTTCGAGGAGATGGTTCGGCGGAGCC 3077

QY 3065 GGAGTAAACAGGTGTTTCCAAACCACTAAAGGGGAAAATGTAACTTTCACTCAGGCT 3124
Db GCCGTGATCAATCCGATCTCAAAACCTTGATGSCAAGATCCTGACTTTTACCCAAATCG 3137
QY 3125 GATAAATTTAGTTAGAGAGAGGGCTTAAGAATGTGAACACCGTTTCATGAGATCCAA 3184
Db GATAAAGAGGCTCTGCTTTCAAGAGGGTATTCAAGATGTTTCACTGTGCTGATGAAGTGCAA 3197
QY 3195 GGAGAAACCTTTGAAGATGTGCGTGGTCAAGTTCAGGCAACTCCACTGACTCTGATT 3244
Db GCGGAGACATACTCTGATGTTTCACTAGTTAGGTTAAACCCCTACACCACTGTTCCGCTCAAGTAC 3257
QY 3245 TCCAACTCTTCCCGCATGTTCTAGTCGCTCTGACTAGACACACAAAGAGCTTTCAAATAT 3304
Db CGAGAGACAGCCACATGTTTGGTTCGATTTGTCAAGGCACACCTGTTCCGCTCAAGTAC 3317
QY 3305 TACACCGTAGTTAGATCTCTTTAGTACAGATAATTTAGTGATTTGTCTTTTAAAGCTCC 3364
Db TACACTGTTGTTATGGATCTTTAGTTAGTATCAATTAGAGATCTAGAGAAACTTAGCTCG 3377
QY 3365 TTCCCTTTAGAAATCTATATGTTAGAGCAGGTAGTATAGCAATTTACAGATGATGCA 3424
Db TACTTGTTAGATATGTAAGGTCTCCAGGCAACAGACCTGATGATTTCTGATATG 3437
QY 3425 GTGTTCAAAGGTCAATACTCTTTTGTGGCAACACCTTAATCAGGAGACTTTCCAGATCTA 3484
Db GGTTCAAAGGTTCCANCTTTTGTTCAGCGCCCAAGACCTGATGAATTTTCTGATGCT 3497
QY 3485 CAGTTCTATTACGATGTATGCTCCCTGGTAAATAGTACTATTAACAAGTATGATGCT 3544
Db CAGTTTACTATGATAAGGTCTCCAGGCAACAGACCTGATGAATTAATTTTCTGATGCT 3557
QY 3545 GTTACATGAGGTAGTGATTAATAGTCTTAATGTGAAGATGTGTTCTTCAATTTTCC 3604
Db GTTACCATGAGGTGACTGACATTTCAATTTGTAAGTGTCAAAAGTGTGCAATTTTGGATATGCT 3617
QY 3605 AAAAGTATTCGATGCCAAGAGGTGAACCATGCTAGAGCCAGTTTGGTACCGCG 3664
Db AAGTCTGTTGCTGGCTTAAGATCAATCAACCACTAATACCTATGTTACGACGGCG 3677
QY 3665 GGGGAACCGCAAGGCTCGAGACTACTCGAAATCTGGTTGCAATGATTAAGAAAT 3724
Db GCAGAAATGCCAGCCAGACTGACTATTGGAAATTTAGTGGCGATGATTAAGAAAGAAC 3737
QY 3725 TTCACGCAACGACCTGACGGGACGATGACATTCAGAGCACCCGATCTGTGTAGTA 3784
Db TTTAACGCCACCGAGTTGTCTGGCATCAATTGATTTGAAATACTGCATCTTTAGTTGTA 3797
QY 3785 GATAAGTATTTGATAGTATTTTATTAAGAAAGAAATACACAAATAATTTGCTGGA 3844
Db GATAAGTATTTGATAGTATTTGCTTTAAGAAAGAAAGAAACCAATTAATAATGTTTCT 3857
QY 3845 GTGATGACGAAGGATTTCAATGATGAGATGGTTGGAAAAACAGGAAGAAGTACTATTGGAC 3904
Db TTGTTTCAGTAGAGAGTCTCTCAATAGATGTTTAGAAAAAGCAGGAACAAGTAAATAGGC 3917
QY 3905 GACTGGCTAACTPACAAATTTTACAGATCTCGCGGCACTCGATCAGTACAGACATGATC 3964
Db CAGCTCGCAGATTTTGATTTTGTAGATTTGCCAGCAGTTGATCAGTACGACACATGAT 3977
QY 3965 AAGGCTCAACCAAAACAGAAATTTGGACCTTTCAATTCAGAACTCAATACCTGCTCTGCAA 4024
Db AAGCAACACCCCAAGCAAAATTTGGACACTTCAATCAACAGGATGATCCCGGTTTGGCAG 4037
QY 4025 ACAATGTCTTACCAATTCGAAGCAGATCAACGGTATTATTTTGGCCGGTTTCT---CAGAGCTT 4081
Db ACGATTTGTGTACTATTCAAAAGATCAATGCAATATTGGCCCGTTGTTTGTAGTGAGCTT 4097
QY 4082 ACAAGTTGCTGTCGAGGCAATTTGATTTCAAGAGATTTCTTTTCTTTTACTAGAAAACT 4141
Db ACTAGGCAATTACTGGACAGTGTGATTTCTGAGCAGATTTTGTGTTTTCACAGAAAGACA 4157
QY 4142 CCAGAACAGATTTCAAGAAATTTTCTCGGATCTCGACTCGCACGTTCTCTATGGATGTGTTA 4201

Db 4158 CCAGCGCAGATTGAGGATTTCTTCGGAGATCTGCACAGTCAATGTGCCGATGATCTGTG 4217
QY 4202 GAACTGGATATTTCTTAAGTATGATAAGTCAAGAACAGAGTTTCAATTTGCTGTAGAGTAT 4261
Db GAGCTGGATATCANAATACGACAAATCTCAGAAATGAATCCCACTGTGCTAGTAGATAC 4277
QY 4262 GAAATATGAAAAAGATTGGGTCTCAATGAGTTTGGCCGAGTGTGGAACCAAGGGCAC 4321
Db GAGATCTGCGCAAGATTGGGTTTGAAGACTTCTTGGGAGAAAGTTTGGAAAAACAGGGCAT 4337
QY 4322 AGAAAAACAACCTTTGAAGGATTAATTTGCTGGAATCAAGATGCTGTGGTATCAAAGG 4381
Db AGAAAGACCACTTCAAGGATTTATACCAGGATATAAAACCTTGCATCTGGTATCAAAGA 4397
QY 4382 AAAAGCGGTGATGTGACTTACTTTCATCGGCAATCTGTTAATAATAGCAGCTTTGCTGGGT 4441
Db AAGACGGGGACGTCAAGACGTTTCAATGGAAACACTGTGATCATTTGCTGCTATTTGGCC 4457
QY 4442 TCAATGTTTACCGATGGAAGAGTCAAAAAGGTGCTTTTGTGGAGACGATTCGCTTTTG 4501
Db TCGATGCTTCCGATCGAGAAAATAATCAAAGGAGCCTTTTGGGTGACGATAGTCTGCTG 4517
QY 4502 TATTTTCCAAAGGGTTTGGATTTCCCTGACATTCAGTCAATGCTAACTCATGTGGAAT 4561
Db TACTTTCCAAAGGGTTGTGAGTTTCCGATGTGCAACACTCCGCGAACTTATGTGGAAT 4577
QY 4562 TTTGAGGCCAACTCTATAGAAAGAGTACGGTTACTTTTGTGGTAGATACATCATACAC 4621
Db TTTGAGCAAAACTGTTTAAAAAACAGTATGATACTTTTGGGAAAGATATGTAATACAT 4637
QY 4622 CATGATAAGGGACAAATAGTGTATTTATGATCTTTTGAAGTTCATCTCCTCAAACTGGGCA 4681
Db CACGACAGAGGTGCTTGTGTTTACGATCCCTAAAGTTGATCTCGAAACTTGTGCT 4697
QY 4682 AAAACATATCAAGGATATGATCATTAGAAAGTTAAAGGTTCTTTTGGCCGATGCTGCT 4741
Db AAAACATATCAAGGATTTGGAAACACTTTGGAGGAGTTTCAAGAGTCTCTTTGTGATGTTGCT 4757
QY 4742 TGTTCTCGTCCGAACTGGTGTCTTAGCTTTTCCGAGCTGAAACGAGCTATCAAGGAGGTT 4801
Db GTTTCTGTT---GAACTTTGCTGTTATACACACAGTTGGACGACGCTGATGGGAGTT 4814
QY 4802 CATAAAAACCGGATGATGTTGCTTTTAAATGTTGTTAAACAAATTTTGTGTGAT 4861
Db CATAGACCGCCCTCCAGTTTGGTTTGTATTAAGGCTGCTGTAAGATTTTGTCTGAT 4874
QY 4862 AAATTTTATTTAGAACTTTGTTTAAATGCTGTAGTCTCAGAGATACTGTCAAAAT 4921
Db AAAGTTCTTTTGAAGTTTGTATATAGATGCTCTAGTTGTTAAAGGAAAGTGAATAT 4934
QY 4922 TAGCGAGTTTCATTTGATCTTTGCAAAACAGGATGAGATCTTCCGCAATTCATGACTAAGGT 4981
Db CAATGAGTTTATCGACCTGACAAAATATGGAAGATCTTACCGTCAATGTTTACCCCTGT 4994
QY 4982 CAAGAGTGTTAGAATATCGACTGTGGACAAGATTTATGGCTGTTAAGAATGATAGTCTTTC 5041
Db AAAGAGTGTATGTTGTTCCAAAGTTGATATAATATGTTTTCATGAGAATGAGTCAATGTC 5054
QY 5042 TGATGTAGATTTTAAAGGTTTAAAGTTAGTTAAGAAGGGTATGTGCTGCTAGCTGA 5101
Db AGAGGTGAACCTTTCTTAAAGGAGTTAAAGCTTATGATAGTGGATACGTTCTGTTTACCGG 5114
QY 5102 TTTGTTAGTGTCTGGGGAGTGGAACTCTCCCGGATAACTCGCGGTGGTGTCTAGTGTGTTG 5161
Db TTTGTTGCTGTCACGGGCGAGTGGAACTTGTGCTGCAATTTGACAGAGGAGTGTAGCGTGTG 5174
QY 5162 TATTTGTAGATAAGAGAAATGAAAAGAGAGTAAAGGAAGCAACGCTGGGTGCTGATCACGCCCC 5221
Db TCTGTTGGACAAAGAGTGAAGAGCCGAGGACCACTCTCGGATCTTCTACTACACAGC 5234
QY 5222 TGCTTCCAAAAAGAAATTTTCTTTTAAAGCTTAATCCCTTAATTTTCAATAACATCCGAGGA 5281

Db 5235 AGCTGCAAGAAAGATTTTCAGTTCAAGGTGTTCCCAATATATGCTATATACCCACCCAGGA 5294
Qy 5282 TGCTGAGAAGCACCCGTGGCAAGTGTGTAGTGAATATCAAGAGAGTGGCTATGGAAGAGG 5341
Db 5295 CGCGATGAAACCTCTGGCAAGTGTGTAGTGAATATGGAAGATGTGAGGCGG 5354
Qy 5342 ATACTGCTCTTATCTTGGAGTTCGTTTCAATTTGTGTAGTACATAAAATATGTAAG 5401
Db 5355 TTTCTGTCGCGTTTCTCTGGAGTTTGTGCGGTGTGTATGTTTATAGAAATAATAAAA 5414
Qy 5402 AAAAGGTTTGAGGAAACGTAATTTTGAAGTGTGACAGAGCGGCTCGCCAAATTTGAATCACTGA 5461
Db 5415 ATTAGGTTTGAGAGAGAGATTACAAACGTGAGAGACGGAGGCGCCATGGAATTTACAGA 5474
Qy 5462 AAAGGTTTGAGAGGTTCTGAGTGAAGTACCAATGCGTGTGAAACTCGAAAAAGGTTTC 5520
Db 5475 AGAAGTCGTTGATGAGTTCATGGAAGATGTCCTATGTGCGATCAGGCTTGCAAAAGTTTC 5533

RESULT 15

US-10-103-327-33
; Sequence 33, Application US/10103327
; Publication No. US20030106095A1
; GENERAL INFORMATION:
; APPLICANT: GARGER, Stephen A.
; APPLICANT: TURPEN, Thomas H.
; APPLICANT: KUMAGAI, Monto H.
; TITLE OF INVENTION: PRODUCTION OF LYOSOMAL ENZYMES IN
; TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
; FILE REFERENCE: 008010087CPUS06
; CURRENT APPLICATION NUMBER: US/10/103,327
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US/09/993,059
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: RastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 11641
; TYPE: DNA
; ORGANISM: Tobacco mosaic virus
US-10-103-327-33

Query Match 36.1%; Score 2291.4; DB 15; Length 11641;
Best Local Similarity 64.0%; Pred. No. 0;
Matches 3532; Conservative 0; Mismatches 1966; Indels 21; Gaps 4;

Qy 20 ACAACAAATTAACAAACAAACAAACATATTACAAACAAACAAACAAACAAACAAACAAAC 79
Db 18 ACCAACACAAACAAACAAACAAACATATTACAAATTTACAAATTTACAAATTTACAAAT 77
Qy 80 ATACAATCTTAATTAAGCAACGCCCTTCTTGAAGCGGTGAGTGTGTAACAAACACTCTCGTT 139
Db 78 ACACAGACAGTACCACATCATGCTTGTGACACTGTCCGAGGAAACAACTCCTCTGTC 137
Qy 140 AATGACCTTCAAGAGCGCATGTACATAGCGCGGTGAGAAATTTAAGCGCGGAC 199
Db 138 AATGATCTAGCAAGCGTCTGCTTTACGACACAGCGGTGGAAGTTTAAACGCTCGTGAC 197
Qy 200 CGTAGACCAAGGTCAACTTTTCAAACTATTAGCAAGCAAGCAAGCGTCTTAGTCTCC 259
Db 198 CGAGGCCAAGGTCAACTTTTCAAGATTAAGCGAGGAGCAGCGTTATTGCTACC 257
Qy 260 AACCGGTACCCGGAGTTCCAGATTACCTTTTATTAATCTCAAAATGCGGTACACAGTTTG 319
Db 258 CGGCGTATCCAGAAATCCAAATTTACATTTTATAACACGCAAAATGCGGTGCAATCGCTT 317
Qy 320 GCTGGAGTTTGAGAGCAATTAAGATTTGAATATCTGATCTACAGTTTCCCTATGGATCG 379
Db 318 GCAGGTGATTTGCGATCTTTAGAACTGGAATATCTGATGATGCAAAATTTCCCTACGGATCA 377
Qy 380 CCGACATATGATAGGTGGAACTTTTCAGACCAATTTGTTCAAAGGCGAGGATTAAGTG 439
Db 378 TTGACTTATGACATAGGCGGAATTTTGCATCGCATCTGTTCAAGGACGAGCATATGTA 437

Qy 440 CATTGCTGTATGCCCAATCTGGACATACGAGATATATGAGGCGACGAGCAAAAGGAC 499
Db 438 CACTGCTGTATGCCCAACCTGGACGTTTCGAGACATCATCGGCACGAAAGGCGCAAAAGAC 497
Qy 500 TCAATTCAGATGTATTGTCCAGATGTCTCGTTCTTAAACAAGGTAAATTCCTGAGTTTCAA 559
Db 498 AGTATTGNACTATACCTTCTAGGCTAGAGAGAGGGGGGAAACAGTCCCAACTTCCAA 557
Qy 560 AGGAGGCTTTTAAACAGGTATGAGAACTCCCAACGAAAGTCTGCTCTCTTAAACCTTTT 619
Db 558 AAGGAAGCAATTCACAGATACGAGAAATTCCTGAAGACGCTGCTCTGCAAACTATTTC 617
Qy 620 CAGGATTCGAATACATCCGCCAGAGAAATAGTGTGTAAGATACGCTGTGCTCTGCAC 679
Db 618 CAGCAATTCGACATCAGCCGATGCAAGCAATCAGGCGAGGTATGCAATTCGCGCTACAC 677
Qy 680 AGTTTGTATGATATTCCTGTGATGAGTTTGGAGCTGCGTTAAATATCTAAGAAATATACAT 739
Db 678 AGCATATATGACATACAGCCGATGAGTTGCGGGCGGCACTCTTGAGAAATATGTCAT 737
Qy 740 GTATGTTATGACGCTTCCATTTTGGCAGAAAGCAATTAATTAAGACGAGAGGAGTTACG 799
Db 738 ACGTGTATGCGGCTTCTCCACTTCTCTGAGAACTGCTTCTTGAAGATTATCATAGTCAAT 797
Qy 800 CTTAATGAATAGCGCAACTTTTCAAAAGAGAGGTGATGATGTTCTTTTCTTTTCTTCT 859
Db 798 TTGGACGAAATCAACGCGTGTCTTCCGCGCATGGAGCAAGTTGACCTTTCTTTTGCAC 857
Qy 860 GATGAAAGTACTTTAAATTAATAGTCATAAAATACAAAATATCTTGCAATATGATGTTAAA 919
Db 858 TCAGAGAGTACTCTTAATTAATGTCATAGTTATTTCTAATATTTCTAAGTATGTCGAAA 917
Qy 920 TCTTACTTCTCTGCTCTAGTAGAATAGTTTACTTTAAGGAATTTTATGACACTAGGGTT 979
Db 918 ACTTACTTCCCGGCTCTAATAGAGAGTTTACATGAAGAGTTTATGAGTCAACAGAGTT 977
Qy 980 AATACTTGGTTTGTAAATTTACCAAGTAGATACCTATATCTGTACAGAGGTGTAGA 1039
Db 978 AATACCTGGTTTGTAAAGTTTCTAGAAATAGATACTTTCTTTGTACAAAGGTGTGGCC 1037
Qy 1040 CAAGTAGGTTGTATGATGATCAGTTCTATGAGCGGATGGAAGACGCTTTTGTCTTACAAG 1099
Db 1038 CATAAAAGTGTAGATAGTAGGACGAGTTTATCTGCAATGGAAGCGCATGSCATTAACAA 1097
Qy 1100 AAAACCTTGGCCATGTTTCAACACTGAAAGAGCAATCTTTAGAGACACGGCTTCGGTTAAC 1159
Db 1098 AAGACTCTTGCATGTGCAACACGAGAGAAATCTCTCTGAGGATTATCATCATAGTCAAT 1157
Qy 1160 TTTTGGTTCCCTAAGATGAAGGACATGCTGATAGTACCGCTGTTTGGGGTCTCTATTACC 1219
Db 1158 TACTGGTTTCCCAAAATGAGGGATATGTTATCATGATCACTATTATTCGACATTTCTTGGAG 1217
Qy 1220 AGCAAAAAGATGACAAGGAGTGAAGTCAATGTTTAAATCGTGAATCTGTTTACACAGTCTT 1279
Db 1218 ACTAGTAAAGAGCGCCAGAGAGTCTTAGTGTCCAGGATTTCTGTTTACAGTCTT 1277
Qy 1280 AATCATATCAGACATATCAAGCCAAAGCGTTAACTTTACAGAACGTTATTTCTTCTG 1339
Db 1278 AACCACATTCGACATACACAGGCGAAAGCTTTCATACATACGCAAAATGTTTGTCTCTGTC 1337
Qy 1340 GAGTCTATAGATCCCGGTGATTAATCAATGTTGTTACTGCTAGGTCTGAATGGATGTA 1399
Db 1338 GAATTCGATCGATCGAGGGTAAATCAITTAACGGTGTGACAGGAGGTCCGAATGGATGTG 1397
Qy 1400 GATAAAGCAATTTCTCAACCTCTGTCATGACTTTCTTTGACAGACTAAGCTGGCTGCG 1459
Db 1398 GACAAATCTTTGTTTACAAATCTTGTCCATGACGTTTACCTGTCATACTAAGCTTGGCGTT 1457
Qy 1460 CTTCAAGACGATATAGTAATGGGAAAGTTTCGGTGTGCTTGGATTAAGACCACTTCTGAAC 1519
Db 1458 CTAAGGATGACTTACTGATTAGCAAGTTTAGTCTCGGTTTCAAAAACGGTGTGCCAGCAT 1517

QY 1520 ATTGGGATGAGTGGCAAAATTTTGGAAAGCTTTTCCCACTATCAAGAGAGATTG 1579
 Db 1518 GTGTGGATGAGATTTTCGCTGGCTTTTGGAAAGCGATTTTCCCTCGGTGAAGAGAGGCTC 1577
 QY 1580 GTGAGCAGGAAATTTCTGGATGATGAGATGCTCTGAAGATCAAGATCCAGATCTG 1639
 Db 1578 TTGAACAGGAAATTTATCAGAGTGGCAGCGCATTTAGAGATCAGGGTGCCTGATCTA 1637
 QY 1640 TATGTCACATGGAAGACAGAGTTGCTAGCTGTAATACACCAAGTCTCAGGAGTTACCGCAT 1699
 Db 1638 TATGTGACCTTCCACGACAGATTAGTACTGATGATCAAGGCTCTGTGACATGCTCGG 1697
 QY 1700 CTAGATATCAAGAGGACTTAGAAGAGCTGAGCAAAATGTCAGACCGCTTATCAGAAATTA 1759
 Db 1698 CTTGACATTTAGGAAGAGATGGAAGAAACCGAAGTGTATGATCAATGCACTTTTCAAGAGTTA 1757
 QY 1760 TCTATCCTTAAGGCTCTGATTAATTTTCGATATCGCAAGTTTCAAGACATGTGCAAGGCT 1819
 Db 1758 TCGGTGTTAAGGAGTCTGACAAATTCGATGTTGATGTTTTCCTCCAGATGTGCCAATCT 1817
 QY 1820 TTAGATGTTAGTCTGATGTGGCAGCACGAGTAATCGTTGCAAGTGGCCGAGAAATAGAAGC 1879
 Db 1818 TTGAAGTGTACCCCAATGACCGCAGCGAAGGTTATAGTCGGGTCAATGAGCAATGAGAGC 1877
 QY 1880 GGTTTAACTCTTACTTTTATAGCCCAACCGAGGAGAAATGTGGCTAAGGCTCT- ----T 1933
 Db 1878 GGTCTGACTCTCACATTTGAAACGACCTACTGAGGCGAATGTTGCGCTAGCTTTACAGGAT 1937
 QY 1934 AAAAGCAGCGGCTCTGAGCGCGTGTATGTTTGAACCGACATCCGAGAGGTGAACGTA 1993
 Db 1938 CAAGAGAAGGCTTTCAAGAGTGTCTTGGTAGTTTACCTCAAGAGAAGTTGAAGAACCGTCC 1997
 QY 1994 AATAAATTTTCTATTTCTGAAAGGAGATTCGCTGTGTGTCAGAAAGTCAATGTTG 2053
 Db 1998 ATGAAGGTTGATGCGCCAGAGAGAGATTACAATAGTGTGTTCTGCGAGATCAATCG 2057
 QY 2054 ACCAATGCTAACTTAGAGCACAGGAGTTGGAGTCCCTCAACGATTTTCCATAGGCTTGC 2113
 Db 2058 GAGTCGCTCTATTCTAAGAACGAGGAGATAGAGTCTTTAGAGCAGTTTTCATATGGCAAG 2117
 QY 2114 GTGGATGATGATTAACAAGCAAAATGGCATTCGGTGTCTACATCTGCTCACTCAAGTT 2173
 Db 2118 GCAGATTCGTTAATTCGTAAAGCAGATCAGCTCGATTTGTGTACACGGGTCCGATTAAGTT 2177
 QY 2174 CAACAAATGAGAACATCTGAGACAGTTTGGCAGCTTCGTTGTCGCCACTGTATCAAAAT 2233
 Db 2178 CAGCAATGAAAACTTTATCGATAGCTGCTGATAGCATCACTATCTGCTCGGTGTGCAAT 2237
 QY 2234 CTATGCAAGTCACTAAAGGATGAAGTCGGGTATGATTTCTGATTTCCAGGGAGAAAGTTGGT 2293
 Db 2238 CTCGTCAAGATCTCAAGATACAGCTGTCTATTGACCTTGAACCCGTCAAAAGTTTGA 2297
 QY 2294 GTTTGGATGTCTATTGAAAAAGTGGCTCCCTCAACCTCGCGCCAAAGGTCAATCG 2353
 Db 2298 GTCTTGGATGTTGCATCTAGAAAGTGGTTAATCAAAACCAACCGGCCAAGATCATGATCG 2357
 QY 2354 GGAATTTCTGATTTACAGGGGAAATGTTTACTGCACTTCTATCTTATGAGGAGAT 2413
 Db 2358 GGTGTTGTTGAACCCACCGGAGAAAGTATCATGTGCGCGCTTTTGGAAATGATGAGCAG 2417
 QY 2414 AGAATGATGATGAGAGCGACTGAGAGGCTGGCTGTATCATCTGATACAAATGGTATAT 2473
 Db 2418 GGTGTGTGATCGCGATGATTGGAGNAGATGAGTGTGAGTCTGAGTCTGAGTCTGTTTAT 2477
 QY 2474 TCTGATATTCCAAGCTCCAAATCTGTAGGAAACCAATGAGAGAGCGGTGAACCCCGAA 2533
 Db 2478 TCCGACATGCGGAACTCAGAACTCTGCGCAGACTGCTTCGAAACCGAGAACCGCATGTC 2537
 QY 2534 CTTACTGCAAGATGTTACTTGTGGATGGGCTGCTGTTGTGGAAAGTACAAAGGAGAT 2593
 Db 2538 AGTAGCGCAAGGTTGTTCTTGTGGACGAGTTCGCGGCTGTGGGAAACCAAGAAAT 2597
 QY 2594 TTTGAAAGATTTGATCTTTGATGAGGATTTGATCTTTGTTCTTCCGMAAACCAAGCTGCTGCT 2653

Db 2598 CTTTCCAGGTTAAATTTTGTGAAGATCTAATTTTAGTACCTGGGAAGCAAGCCGGA 2657
 QY 2654 ATGATCAGAAGAGGCTAAATTCATCTGACTGATAAGAGCCCAATGCAATGCAATGTGAGA 2713
 Db 2658 ATGATCAGAAGAGGCTGCAATTTCTCAGGATATTTGTGCCCCAGNAGCAACGTTAA 2717
 QY 2714 ACGGTAGATTCTCTTAATGAT- ----CCAAAACCGCGATCAACAAGAGGCTT 2764
 Db 2718 ACCGTTGATTTCTTTCATGATGAATTTTGGAAAAAGCACACGCTGTCAAGAGTTA 2777
 QY 2765 TTTATTTGATGAGGTTGATGCTGCACACCGCTGTGTTAACTTCTCTGCTGCTTATCTCT 2824
 Db 2778 TTTATTTGATGAGGTTGATGTTGATCTACTGTTGTTGTTAAATTTCTTGTGGCGATGTC 2837
 QY 2825 GGTTCGCATCCGATACATTTTACCGAGATACACAGCAGATTCCTTTTCAATTAACAGATT 2884
 Db 2838 TTTGCGGAATTTGATATGTTTACCGAGACACACAGCAGATTCATACATCAATAGATT 2897
 QY 2885 CAGAAATTTCCGATATCCCAACATTTTGAAGAGCTGCAAGTGGATGAAGTTGAGATGAGG 2944
 Db 2898 TCAGGATTTCCGTTACCCGCTTTCGCAATTTGCAAAATTTGAAGTTGACGAGGTGAGACACG 2957
 QY 2945 AGACCACTGAGATGCCAGGTGATGTAATTTTCTTACATCGAAGTACGAGGA 3004
 Db 2958 AGAATCTACTCTCGTTGTCAGCGCATGTCACATTTATCTGAACAGGAGATATGAGGCG 3017
 QY 3005 GCGGTGACAAACCACTTCAACTGTCAACCGATCGCTCATCTGAGATGATAGCGGTAAG 3064
 Db 3018 TTTGTATGAGCAGCTCTTTCGTTTAAAGTCTGTTTCGAGGAGATGTTGCGCGGAGCC 3077
 QY 3065 GGAGTACTAAACAGTGTTCCAACCACTTAAAGGAAATTTGTAATCTTTCATCTAGGCT 3124
 Db 3078 GCGGTGATCAATCCGATCTCAAAACCTTTCGATGCGAAGATCTGACTTTTACCCAACTG 3137
 QY 3125 GATAAATTTGATGAGGAGAGAGGCTATAGAAATGTGAACCGCTTCATGAGATCCAA 3184
 Db 3138 GATAAAGAAAGCTCTGCTTTCAAGAGGATTTCAAGTGTTCACACTGTGATGAAGTGC 3197
 QY 3185 GGAGAAACCTTTGAAGATGCTGCTGCTGATTCAGATTCAGCGCAACTCCACTGACTCTG 3244
 Db 3198 GCGGAGACATCTCTGATGTTTCACTAGTTAGTTAAACCTTACACAGTCTCCATCAT 3257
 QY 3245 TCCAGTCTTCCCGCATGTTCTAGTCTGCTGCTGATGACACACAAAGAGCTTCAATAT 3304
 Db 3258 GCAGGAGACAGCCACATGTTTGTGCTGCAATGTCGCAAGGACACCTGTTGCTCAAGTAC 3317
 QY 3305 TACACCGTATGTTAGATCCTTTAGTACAGATTAATTTAGTGAATTTGCTTCTTTAAGCTCC 3364
 Db 3318 TACACTGTTGTTATGATCCTTTAGTTAGTATCATTTAGAGATCTAGAGAACTTAGCTCG 3377
 QY 3365 TTTCTTTTGAATGATATGTTAGAGCAGGTTAGTAGCAATTTACAGATGGATGCA 3424
 Db 3378 TACTTGTAGATGATTAAGGTCGATGAGGACACATAGCAATTTACAGATGACTCG 3437
 QY 3425 GTGTTCAAAAGGTCATTAATCTTTTGTGGCAACCTTAAATCAGGAGACTTTCAGATCTA 3484
 Db 3438 GTGTTCAAAAGTTCCTTCTTTTGTGAGCGCCAAAGACTGCTGATATTTCTGATG 3497
 QY 3485 CAGTTCTTATGATGATGCTCCCTGTTATAGTACTATCTTACAAAGTATGATGCT 3544
 Db 3498 CAGTTTACTATGATGATGCTCCAGGCAACAGCACCATGATGATTAATTTTGTGATGCT 3557
 QY 3545 GTTACCATGAGTTACGTGATTAATGCTTAAATGTGAAGATGTTGTTTGTGATTTTTC 3604
 Db 3558 GTTACCATGAGTTGATGATTTTCAATTTCAATGTCAGATTTGATTTGATGATGCT 3617
 QY 3605 AAAAGTATTTCCGATGCAAGGAGGTTGAAACCAATGCTAGAGCCAGTTTTCGTAACGCG 3664
 Db 3618 AAGTCTGTTGCTGCGCTTAAGGATCAATCAAAACCACTAATCTATGTTGACGCG 3677
 QY 3665 GCGGAACCGGCAAGGCTGAGGACTCTCGAAAAATCTGTTGCAATGATTAAGAAAT 3724

Db 3678 GCAGAAATGCCACGCCAGACTGGACTATTGGAAATTTAGTGGCGATGATTAAAGGAAC 3737
Qy 3725 TTCAACGCCACAGACCTGACCGGGACCGATTGACATTTGAGAGCACCGCATCTGTTGTAGTA 3784
Db 3738 TTTAAACGCCCGAGTGTCTGGCATCATTGATTTGAAATACTGCGCATCTTTAGTTGTA 3797
Qy 3785 GATAAGTTTTTGTAGTAGCTATTTTATTAAGAAAGAAAATACACAAAAATATTGCTGGA 3844
Db 3798 GATAAGTTTTTGTAGTAGTTATTCTTTAAAGAAAAGAAAACCAAAATATAAAATGTTTCT 3857
Qy 3845 GTGATGACGAAGGATTCAAATCATCAGATGGTTGGAAAACAGAAAGAGTACTATTGAC 3904
Db 3858 TTGTTTCTAGTAGAGTCTCTCATAATAGATGGTTAGAAAAGCAGGTAACAAATAGGC 3917
Qy 3905 GACTTGGCTAACTACAAATTTTACAGATCTGCCGCCATCGATCAGTACAAGCACATGATC 3964
Db 3918 CAGCTCGCAGATTTTGTATTTTGTAGATTGTCAGCAGTGTGATCAGTACAGACACATGATT 3977
Qy 3965 AAGGCTCAACCAAAACAGAAATTTGACCTTTCAATTCGAAATGAATACCCCTGCTCTGCA 4024
Db 3978 AAAGCACAAACCAAGCAAAAATTTGGACACTTTCAATCCAAACCGAGTACCCGGCTTTGCG 4037
Qy 4025 ACAATTTGTTTACCAATTCGAACAGATCAACGGTATTTTGGCCGGTTTCT---CAGAGCTT 4081
Db 4038 ACGATTGTGTACCAATTCAAAAGATCAATGCAATATTTGGCCGGTTGTTTAGTGAGCTT 4097
Qy 4082 ACAAGTTGTGCTCGAGGCAATTTGATTTCTAAGAAGTTTCTTTTCTTACTAGAAAAC 4141
Db 4098 ACTAGGCAATTTACTGGACAGTGTGATTCGAGCAGATTTTGTGTTTTCACAAAGAAAGACA 4157
Qy 4142 CCAGAACAGATTTCAAGAAATTTTCTCGGATCTCGACTCGACGTTCTATGGATGTGTTA 4201
Db 4158 CCAGCGCAGATTGAGGATTTCTTCGGAGATCTCGACAGTCAATGTGCCGATGGATGTCTTG 4217
Qy 4202 GAACTGGATATTTCTAAGTATGATAAGTCAGAACAGATTTTCAATGTGCTGTAGAGTAT 4261
Db 4218 GAGCTGGATATTAAGAAATACGACAAATCTCAGAAATGAAATTCCTGTGCGATGAAATAC 4277
Qy 4262 GAAATATGAAAAGATTGGGTCTCAATGAGTTTGTGGCCGAAGTGTGGAAAACAAGGGCAC 4321
Db 4278 GAGATCTGGCAGATGGGTTTTGAAAGACTTTCTGGGAGAAGTTTGGAAAACAAGGGCAT 4337
Qy 4322 AGGAAACAACTTTGAAGGATTTACATTTCTGGATCAAGACATGCTGTGTATCAAAAG 4381
Db 4338 AGAAAGACCAACCTCAAGGATTTATACCGCAGGTATAAAAACCTCGCATCTGGTATCAAGA 4397
Qy 4382 AAAACGGTGTGATGACTACTTTTCAATCGCAATACTGTTATAATAGCAGCTTGTCTGGGT 4441
Db 4398 AAGACGGGGACGTACGACGTTTCAATGGAAACACTGTGATCATTTGCTGCATGTTTGCC 4457
Qy 4442 TCAATGTTTACCGATGGAAAAGGTATATAAAGGTGCTTTTGTGGAGACGATTCGGTTTTG 4501
Db 4458 TCGATGCTTCGATGGAGAAAATAATCAAGGAGCCTTTTTCGGGTGACGATGCTGCTG 4517
Qy 4502 TATTTTCAAAAGGGTTTGGATTTCCCTGACATTCAGTCATGTGCTAATCTCATGTGGAAT 4561
Db 4518 TACTTTCAAAAGGGTTGTGAGTTTTCGGATGTGCAACACTCCCGCAATCTTATGTGGAAT 4577
Qy 4562 TTTGAGGCCAACTGTATAGAAAGGTTACCGGTTACTTTTGTGTAGATACATCATACAC 4621
Db 4578 TTTGAGGCCAAACTGTTTAAAAACAGTATGATACATTTTTCGGAGAGATGTAATACAT 4637
Qy 4622 CATGATAAGGAGCAATAGTGTATTAATGATCCTTTGAAATTTGATCTCAAACTTTGGGCA 4681
Db 4638 CACGACAGAGATGCTATGTTGTAATTACGATCCCTCAAGTTGATCTCGAAAACCTTGGTGCT 4697
Qy 4692 AAAATATCAAGGATTAATGATCACTTAGAAGATTAGGGTGTCTTTGTGCGATGTTGCT 4741
Db 4698 AAAACATCAAGGATTTGGGAAACACTTTGGAGAGTTTCAAGAGTCTCTTTGTGATGTGCT 4757
Qy 4742 TGTTTCGCTCGGAAACTGTGTAGCTTAGGCTTTCCGAGCTGAACCGAGCTTCAAGGAGGTT 4801
Db 4758 GTTTCGTT--GAACAAATTTGCGGTATTATACACAGTTGGACGCGCTGTATGGAGGTT 4814

Qy 4802 CATATAAACCCCGATTTGATGTTTGGTTTGGTTCTTTTAAATTTGTTTAACAAATTTTGTGTGAT 4861
Db 4815 CATAAGACCCCCCTCCAGGTTCTGTTTGTATATAAAAGTCTGGTGAAGTATTTTGTCTGAT 4874
Qy 4862 AAATTTTTATTAGAACTTTTGTATTTTAAATGGCTGTTAGTCTCAGAGATATCTGTCAAAAT 4921
Db 4875 AAAGTTCTTTTATAGAGTTTGTATTATAGATGGCTCTAGTTGTTTAAAGGAAAAGTGAATAT 4934
Qy 4922 TAGCGAGTTTCATTTGATCTTTTCGAAAACAGGATGAGATACCTTTCCGGCATTTCAATGAAGGT 4981
Db 4935 CAATGAGTTTATCGACCTGACAAAATGGAAGAGATCTTACCGTCCGATGTTTACCCCTGT 4994
Qy 4982 CAAGAGTTTGAAGATATCGACTGTGGACAAGATTAATGGCTGTTTAAAGATGATAGTCTTTC 5041
Db 4995 AAAGAGTGTATGTGTTTCCAAAGTTGATAAAATAATCGTTTCATGAGAATGAGTCATTTGTC 5054
Qy 5042 TGATGTAGATTTTACTTAAAGGTGTTTAAAGTTAGTTTAAAGAAAGGTTATCTGTGCTTAGCTGA 5101
Db 5055 AGAGGTGAACCTTCTTAAAGGAGTTAAGCTTATTGATAGTGGATACGTCGTGTTTAGCCGG 5114
Qy 5102 TTTGGTAGTGTCTGGGAGTGGAACTCTCCCGGATAACTGCCGTGGTGTGTCAGTGTTTG 5161
Db 5115 TTTGGTCTGTCACGGCGAGTGGAACTTGGCTGACAAATTCAGAGAGAGGTGTGAGCGTGTG 5174
Qy 5162 TATTGTAGATAAGAGATGAAAAGGAGTAAGGAAGCAACGCTGGGTGCGTATCACGCCCC 5221
Db 5175 TCTGGTGGACAAAAGGATGGAAAGAGCCGAGGCCACTCTCGGATCTTACTACACAGC 5234
Qy 5222 TGCTTGCAAAAAGAAATTTTCTTTTAAAGCTAAATCCCTAAATTTTCAATAACATCCGAGGA 5281
Db 5235 AGCTGCAAGAAAGATTTTCAAGTTCAGTTTCAAGGTCGTTCCCAATTTATGCTATTAACCCACCGGA 5294
Qy 5282 TGCTGAGAAGCACCCGTGGCAAGTGTAGTCAATATCAAAAGGAGTGGCTATGGAAGAGG 5341
Db 5295 CGCGATGAAAACGCTCTGGCAAGTTTGTAGTTAATATTAGAAAATGTAAGATGTGAGCGG 5354
Qy 5342 ATACTGCTTTTATCTTTGGAGTTCGTTTCAATTTGTGTAGTACATAAAAAATATGTAAG 5401
Db 5355 TTTCTGTCGCTTCTCTGGAGTTTGTGCGGTGTGTATTGTTTATAGAAAATAATAAA 5414
Qy 5402 AAAAGGTTTTCAGGGAACGTTATTTTGTAGTGTGACAGCGGCTCGCAATTTGAACCTCACTGA 5461
Db 5415 ATTAGGTTTGAGAGAGAAAGATTACAAACGTGAGAGACGAGGCGCCATGGAACTTACAGA 5474
Qy 5462 AAAAGTTGTTGAGGAGTTCGTTGATGAAGTACCAATCGCTGTGTGAACCTCGAAAAAGGTTTC 5520
Db 5475 AGAAGTCGTTGATGAGTTTCATGGAAGATGTCCTTATGTCGATCAGGCTTGCAAAAGTTTC 5533

Search completed: July 28, 2005, 18:44:30

Job time : 2474.02 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 28, 2005, 08:29:34 ; Search time 517.084 Seconds
(without alignments)
15733.537 Million cell updates/sec

Title: US-09-551-494-5_COPY_534_5505
Perfect score: 4972
Sequence: 1 ctaacaaggaattcctcgag.....tgaagtaaccaatggctgtga 4972

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2034.2	40.9	6395	3	US-09-259-741-1
2	2034.2	40.9	6395	3	US-09-037-751-1
3	2034.2	40.9	6395	3	US-09-466-422-1
4	2034.2	40.9	6395	4	US-09-962-527-1
5	2034.2	40.9	6439	3	US-09-259-741-2
6	2034.2	40.9	6439	3	US-09-037-751-2
7	2034.2	40.9	6439	3	US-09-466-422-2
8	2034.2	40.9	6439	4	US-09-962-527-2
9	2031	40.8	6395	2	US-08-687-559-2
10	2031	40.8	6395	4	US-09-401-415-2
11	2031	40.8	6425	3	US-09-259-741-3
12	2031	40.8	6425	3	US-09-037-751-3
13	2031	40.8	6425	3	US-09-466-422-3
14	2031	40.8	6425	4	US-09-962-527-3
15	2031	40.8	6446	3	US-09-259-741-5
16	2031	40.8	6446	3	US-09-037-751-5
17	2031	40.8	6446	3	US-09-466-422-5
18	2031	40.8	6446	4	US-09-962-527-5
19	2031	40.8	6475	3	US-09-259-741-4
20	2031	40.8	6475	3	US-09-037-751-4
21	2031	40.8	6475	4	US-09-466-422-4
22	2031	40.8	6475	4	US-09-962-527-4
23	2029.4	40.8	7685	3	US-09-502-710-22
24	2029.4	40.8	7685	3	US-09-502-710-25
25	2029.4	40.8	7685	3	US-09-502-711-22
26	2029.4	40.8	7685	3	US-09-502-711-25
27	2029.4	40.8	7685	4	US-09-565-616A-1

28	2029.4	40.8	7686	3	US-09-502-710-23
29	2029.4	40.8	7686	3	US-09-502-711-23
30	2029.4	40.8	7687	3	US-09-502-710-24
31	2029.4	40.8	7687	3	US-09-502-711-24
32	2029.4	40.8	7688	3	US-09-502-710-27
33	2029.4	40.8	7688	3	US-09-502-711-27
34	2026.2	40.8	7686	3	US-09-502-710-26
35	2026.2	40.8	7686	3	US-09-502-711-26
36	2026.2	40.8	7686	4	US-09-565-616A-2
37	2026.2	40.8	7926	3	US-09-500-554-1
38	2026.2	40.8	7926	3	US-09-726-648-1
39	2026.2	40.8	7926	4	US-10-119-330-1
40	693.2	13.9	1425	1	US-08-488-672-4
41	690	13.9	1425	1	US-08-708-354-4
42	286.4	5.8	2173	2	US-08-553-619B-6
43	263.2	5.3	1825	1	US-08-176-414B-1
44	263.2	5.3	1825	2	US-08-336-724-1
45	260.8	5.2	807	4	US-09-565-616A-3

ALIGNMENTS

RESULT 1
US-09-259-741-1
; Sequence 1, Application US/09259741
; Patent No. 6033895
; GENERAL INFORMATION:
; APPLICANT: GARGER, STEPHEN
; APPLICANT: HOLTZ, R. BARRY
; APPLICANT: MCCULLOCH, MICHAEL
; APPLICANT: TURPEN, THOMAS
; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
; TITLE OF INVENTION: PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES FROM PLANT
; TITLE OF INVENTION: SOURCES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/259,741
; FILING DATE: February 25, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/037,751
; FILING DATE: March 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 00801.0140.US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-463-8100
; TELEFAX: 650-463-8400
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6395 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic RNA
; US-09-259-741-1

Query Match 40.9%; Score 2034.2; DB 3; Length 6395;


```
Db 4854 CUGUGAAGUUAUUGUCGUAAGAAUUCUUUUUAGAAGUUUUUAUAGUUGGCUUAGU 4913
Qy 4368 TCTCAGAGATCTGTCAAAATTTACGAGTTTCATTGATCTTTTCGAAACAGGATGAGATACT 4427
Db 4914 UGUUAAAGGAAAGAGUAAUACAUGAGUUUAUCGACCUCAAAUUGGAGAGAAUUCU 4973
Qy 4428 TCCGGCATTCATGATCAAGGTCAAGAGTGTGTAGAAATATCGACTGTGGCAAGATATATGGC 4487
Db 4974 ACCGUCGAUGUUUACCCCGUAAAGAGUGUUUUGUUCUCCAAAGUAGUAAUAAUUGGU 5033
Qy 4488 TGTTAAGATCATAGTCTTTCTGATGTAGATTCTTATAGGTTTAAAGTTAGTTAAGAA 4547
Db 5034 UCAUGAGAAGUAGUUAUGCAGAGGUAACCUUUAAGGAGUUAAGCUUAUUGUAG 5093
Qy 4548 AGGTATGTGTGCTTAGCTGATTTGGTAGTGTCTGGGGAGTGGAAATCTCCCGGATAACTG 4607
Db 5094 UGGAUACGUCUUGUUUAGCCGUAUUGGUCUCACGGGCGAGUGGAAUUGCCUGACAAUUG 5153
Qy 4608 CCGTGTGTGTCTAGTGTGTGTATTTGTAGATAAGAAATGAAAGAGTAAAGGAAGCAAC 4667
Db 5154 CAGAGGAGGUGAGCGGUGUGUCUGUGGACAAAGGAUUGGAAAGAGCGACGAGGCCAC 5213
Qy 4668 GCTGGGTGCTGTATCACGCCCTGCTTGCAGAAAGAAATTTCTTTTAAAGCTAATCCCTAA 4727
Db 5214 UCUCGGAUUCUUAACACAGCAGCAGCUGCAAGAAAGAAUUAUUCAGUUAAGGUGUCCCAA 5273
Qy 4728 TTATTCAATAACATCCGAGGATGCTGAGAACACCCGCGCAAGTGTAGTGAATATCAA 4787
Db 5274 UUAUGCUUAACACCCAGCGGAGUAAAGAAACGUCUGGCGAGUUUAUUAUUAUAG 5333
Qy 4788 AGGAGTGCTATGAAGAAGGATATCTGCTTTTATCTTTTGGAGTTCGTTTCAATTTGCT 4847
Db 5334 AAUUGAAGAGUAGUCAGCGGUUUCUGUCCGUUUCUGGAGUUUUGUGCGUGUGUUAU 5393
Qy 4848 AGTACATAAATAATGTAGAAAGGTTTTCAGGGAAGCTATTTTGTAGTGTGACAGCGG 4907
Db 5394 UGUUUAUAGAAUUAUUAUUAUUAUUGGUUUGAGAGAGAAUUAUUAACACGUGAGAGCGG 5453
Qy 4908 CTCGCCAATGAACCTCACTGAAAGGTTGTGTGAGGAGTTCTGTGATGAAGTACCAATGGC 4967
Db 5454 AGGCCCAUGGAACUACAGAGAAGUUGGUUGAGUUAUGAUGGAAGUCCUUAUGUC 5513
Qy 4968 TGTGA 4972
Db 5514 GAUCA 5518
```

```
RESULT 2
US-09-037-751-1
; Sequence 1, Application US/09037751
; Patent No. 6037456
; GENERAL INFORMATION:
; APPLICANT: GARGER, STEPHEN
; APPLICANT: HOLTZ, R. BARRY
; APPLICANT: MCCULLOCH, MICHAEL
; APPLICANT: TURPEN, THOMAS
; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
; TITLE OF INVENTION: PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
; TITLE OF INVENTION: FROM PLANT SOURCES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,751
; FILING DATE: 10-MAR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 00801.0140.999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-463-8109
; TELEFAX: 650-463-8400
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6395 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic RNA
US-09-037-751-1
```

```
Query Match 40.9%; Score 2034.2; DB 3; Length 6395;
Best Local Similarity 44.4%; Pred. No. 0;
Matches 2214; Conservative 957; Mismatches 1793; Indels 21; Gaps 4;

Qy 6 AAGTAAATTCCTCAGTTTCAAGGGAGGCTTTTAAACAGGTATGCAGAAAGCTCCCAACGAA 65
Db 537 AAAACAGUCCCAACUCCAAAAGGAAGCAUUGACAGAUCCGACAGAAUUCUGAAGAC 596
Qy 66 GTCTGCTGCTCTAAAACCTTTTCAGGATTTGTCGAATATCATCCGCCAGAGAATAGTGGTAGA 125
Db 597 GCUGUCUGACAAUACUUCAGACAAUGCCGACAUCCGCGAUGCAUACAGGCGAGA 656
Qy 126 AGATACGCTGTTCTCTGCACAGTTTGTATGATATTCCTGTGATGATGTTGGAGCTGCG 185
Db 657 GUGUAGCCAUUGCGGUACACAGCAUAUAGCAUACACCGCCGAGUAGUUGCGGCGGCA 716
Qy 186 TTAATATCTAAGAAATATACATGTATGTATGTCAGCTTCCATTTTGGCAGAGCATATTATTA 245
Db 717 CUCUUGAGGAAAAGUCCAUACGUGUAUUGCCGUUUCACUUCUCCGAGAACCCUUCU 776
Qy 246 CTAGACCAGACGGAGTTACGCTTAAATGAAATAGGCGCAACTTTCAAAAGAGAGAGTGTAT 305
Db 777 CUUGAAGAUCAUACGUCAAUUUGGACGAAAUCAACGCGUGUUUUUCGCGCGAGAGAC 836
Qy 306 GATGTTCTTTTCTTTGCTGTGATGAAAGTACTTTTAAATTTAGTCTATAATAACAAAT 365
Db 837 AAGUUGACCUUUUUUGCAUCAGAGAGUACUUAUUAUUGUUAUUGUUAUUCUUAU 896
Qy 366 ATCTTGCAATTATGTAGTTAAATCTTACTTTCTCTCTTAGTAGAAATAGTTTACTTTAAG 425
Db 897 AUUCUUAAGUUGUGUCAAACUUAUUCGCGCCUUAUAGAGAGAGUUUAUAGUAG 956
Qy 426 GAATTTTCTACTAGGTTAAATACCTTGTGTTTGTAAATTTTACAAAGTAGATACCTAT 485
Db 957 GAGUUUUUAGUACCAAGUUAUUAUCCUGGUUUUUAAGUUUUUUAAGAAUUAUUAUUAU 1016
Qy 486 ATTCTGTACAGAGTGTTAGACAAGTAGGTGTGATGATGATGATGATGATGATGATGATG 545
Db 1017 CUUUUGUACAAAGGUGUGGCCCAUAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1076
Qy 546 GAAGACGCTTTGCTTACAAAGAAAACTTGGCCCATGTTTCAACACTGAAAGAGCAATCTTT 605
Db 1077 GAAGACCGCAUGCAUUAACAAAGACUUAUUGCAUUGCAUUGCAUUGCAUUGCAUUGCAU 1136
Qy 606 AGAGACACGGCTTCGGTTAACTTTTGTTCCTTAAGATGAAGGACATGTTGATGATGATG 665
Db 1137 GAGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1196
Qy 666 CTGTTTGAGGGTCTTATTACCAGAAAAAGATGACAGGAGTGTAGGTCATTGTTTAATCGT 725
```


Db 1197 UUAUUCGCAUUCUUUUGGAGACUAGUAAGAGGACGCGCAAGAGAGUUCUUAUGUCCAAAG 1256
QY 726 GACTTCGTTTACACAGTGGCTTAATCATATACAGACATATCAAGCCAAAGCGTTAACTTAC 785
Db 1257 GAUUCUGUGUUUACAGUGCUUUAACCAUCCAGAAACAUACCCAGCGAAAGACUUAUACAUAC 1316
QY 786 CAGAACGCTATTATCTTTCTGGGAGTCTATAAGATCCCGGCTGATATCAATCAATGGTGTACT 845
Db 1317 GCAAAUGUUUUGUCCUUGCGAUAUCGAUUCGAGCGGUAUUAUUAUAAACGUGUGACA 1376
QY 846 GCTAGTCTGAATGGATAGATAAGCAATCTTCAACCCCTTGTCAATGACTTTCTTC 905
Db 1377 GCGAGUCCGAAUGGAGUGGACAAUUCUUUUAUCAAUCCUUGUCCAGUACGUAUUAAC 1436
QY 906 TTGCGAGACTAAGCTGCGCTTCAAGACGATATAGTAATGGGAAAGTTTCGCTGCTTG 965
Db 1437 CUGCAUAUACGUCGCGCCUUAUAAAGGAUACUUAUGAUGAUGAUGAUGAUGAUGAUGAUG 1496
QY 966 GATAAGACCACTTCTGAACTTATTTGGGATGAGGTGGGCAAAATTTTGGGAAACGTTTTTC 1025
Db 1497 UCGAAAACGUGUGCCAGUGUGGAGUAGAUUUCGCGGCUUUGGGAACGCAUUA 1556
QY 1026 CCCACTATCAAGAGAGATTGGTACAGGAAATTTCTGGATGTAGTGAGAAATGCTCTG 1085
Db 1557 CCGUCGUGAAAGAGAGACUCUUGAACAGGAAACUUAUCAGAGUGGCGAGCGCAUUA 1616
QY 1086 AGATCMAGATCCAGATCTGTATGTCATGGAAGACAGGTTCTGTAGCTCAATACACC 1145
Db 1617 GAGUACAGGUGGCUUUAUUGUACCUUCCAGCAGAUUAGUGACUGACUGAUAACAG 1676
QY 1146 AAGTCTGAGGATTACCGCATCTAGATATCAAGAAAGCACTTAGAAGAACTGAGCAAAATG 1205
Db 1677 GCCUCUGGACAUGCCGCGUUGACAUUAGGAAAGAUUGAAGAAACGGAUGAUG 1736
QY 1206 TAGACGCGTTATCAGAAATATCTATCTTAAAGGCTGTGATAATTTTGGATATCGGAAG 1265
Db 1737 UACAAUGCAUUCAGAGUUAUCGUGUUAAGGAGUCUGACAAAUUUCGUGUUGAUGU 1796
QY 1266 TTCAAAGACATGCAAGGCTTTAGATGTTAGTCTGTGTCGACGACGAGTATCGTT 1325
Db 1797 UUUUCCAGAUUGCCAAUUCUUUGGAAUGUAGCCCAAGCAGCGGAGGUAUUAUG 1856
QY 1326 GCAGTGGCGAGAAATAGAGCGGTTTAACTCTTACTTTTGAAGCAACCGAGGAGAAAT 1385
Db 1857 GCGUACUAGACMAUGAGAGCGGUCUGACUCUCAUUAUAGCAACCUACUGAGGCGAAU 1916
QY 1386 GTGGCTAAGGCTCT-----TAAAGCACGCGGTCTGAGCGCGTGTATGTCTTGAAACG 1439
Db 1917 GUUGCGCUAGCUUUAACAGGAUUAAGAGAGGCUUCAGAGGUGCAUUGUAGUACCUCA 1976
QY 1440 ACATCCGAAGAGGTGAACGTAAATTTTCTATTTCTGAGAAAGGAGATGTCCTGTG 1499
Db 1977 AGAAGAUUUAAGAACCGUCCAUAGAGGUGUUGAUGGCGCAGAGGAGUUAUCAAUAGCU 2036
QY 1500 TGTGCAAGAAAGTTCATGTTTGAAGATGCTAACTTAGACACCGAGGTTGAGTCCCTC 1559
Db 2037 GGUUUGUGGAGAUCAUCCGAGUGUCUUAUUAAGAACAGAGAGUAGUGUUA 2096
QY 1560 AACGATTTCCATAAGGCTTTCGCTGGATGTGTGATTAACAAGCAAAATGGCATCGGTTGTC 1619
Db 2097 GAGCAGUUAUUAUGCGGACGCGCAGAUUCGUUAAUUGUAAGCAGAUAGGUGCUAUGUG 2156
QY 1620 TACACTGGCTCACTAAAGTTTCAAAATGAAGAACTATGTGGACAGATTTGGCAGTTCCG 1679
Db 2157 UACACGGGUCGAAUUAAGUUCAGCAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2216
QY 1680 TTGTCGCGCACTGTATCAATCTATCAAGTCACTAAAGATGAAGTCCGGTATGATTTCT 1739
Db 2217 CUUUCUGUGCGGUGGUAUUCUGUUAAGAUCCUUAAGAUUUAUUAUUAUUAUUAUUAUUA 2276
QY 1740 GATTTCCAGGAGAAAGTGTGGTGTGTTGGGATGTCACTTTTGAAAGAGTGGCTCTCAAACT 1799

Db 2277 GAAACCCGCUCAAAAGUUUUGGAGUUCUUGAUGUUGCAUUCAGGAAGUGUUAAUCAAACA 2336
QY 1800 GCGGCCAAAGAGTCTATCTATGGGGAGTTGTCTCTGGATTACAAAGGGGAAATTTTATCTCA 1859
Db 2337 AGGCCCAAGAGUUAUGAUGGUGGUGUUGUAGAAACCCAGCGAGGAUAUUAUGUGGCG 2396
QY 1860 CTTTCTATCTTATGAAGAGAGATAGAAATGGTACTGAGAGGACTGAGAGGAGGTGGCTGTA 1919
Db 2397 CUUUGGAUAUUAUGAUGAGCAGGUGUGUGAUGCAUGCAUUGGAGAGAGAGUAGUGU 2456
QY 1920 TCATCTGTATACATGCTATTTCTGATATTGCAAAAGCTTCAAAATCTGAGGAGAAACAATG 1979
Db 2457 AGCUCUGAGUCUUGUUUUUUAUCCACAGUCCGGAACUUCAGAAACUCUGCGCAGACUGCUU 2516
QY 1980 AGAGACGCTGAACCCACGAACTTACTGCAAAAGATGGTACTTTGTGGATGGGTGCTGTG 2039
Db 2517 CGAAACGAGAAACCGCAUGACAGUAGCGAAAGGUUUGUUGGAGCGAGUCCGGGC 2576
QY 2040 TGTGAAAGATGACAAAGGAGATTTTGAAGATTTTGAATCTTGTGAGGATTTTGTCTGTT 2099
Db 2577 UGUGGAAACCAAGAAAUUUCUCCAGGGUUAUUAUUAUGAAGAAUCAAUUUAUUA 2636
QY 2100 CCGGAAACAGCTGCTGCTATGATCAGAAAGGGCTAATTCATCTCGACTGATAACA 2159
Db 2637 CUUGGAGACGCGCGGAAUAGUACAGACCGUGCGAAUUCUCAGGGAUUAUUG 2696
QY 2160 GCCAATGGAACAATGTGAGAACGCTAGATTCACTTCTTAATGCAT-----CCAAA 2210
Db 2697 GCCACGAGGACACGUAUAAACCGUAGAUUUAUUAUGAUAUUAUUGGAAAGACACA 2756
QY 2211 CCGCATCACACAGAGGCTTTTATGATGAAGGGTGTGCTGACACCCGTTGTGTT 2270
Db 2757 CGCUCGACUUAUUAAGGUAUUAUUAUGAAGGUAUUAUGUUGCAUUCUGUUGUGU 2816
QY 2271 AACTCTCTGCTGCTTATCTCTGTTGCGACATCGCATACATTTACGAGATACACAGCAG 2330
Db 2817 AAUUAUUGGCGGAGUUAUUGGAAUUAUGCAUUGUUAUUGGAGACACACAGCAG 2876
QY 2331 ATTCCTTTTCAATAACAGAGTTTCAGAAATTTCCCGTATCCCAAACTTTTGAAGAGTGC 2390
Db 2877 AUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2936
QY 2391 GTGGATGAAGTTGATGAGGAGGACCACTGAGATGCCAGGCTGTGATGATTTTTC 2450
Db 2937 GUUGACGAGGUGAGACACGAGAAACUACUCUCCGUGUCCAGCGCAUGUCAUUAU 2996
QY 2451 CTACATCGAAGTACGAGGAGCGGTGACCACTTCACTGTAACGATCGGTCTCA 2510
Db 2997 CUGAACGAGAGAUUAGGCGCUUUGUCAUGAGCAUUCUUCGUAUUAUUAUUAUUAUUA 3056
QY 2511 TCTGAGATGATAGCGGTAAGGGAGTACTAAACAGTGTTCACAAACCACTAAAGGGA 2570
Db 3057 CAGGAGUUGGUGCGGAGCGCCCGUGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3116
QY 2571 ATTTGAATTTTCACTCAGGCTGATTAATTTTGAAGTTAGAGAGAGGCTTATGAATGTG 2630
Db 3117 AUCCUGACUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3176
QY 2631 AACACGTTCTAGATCCAGAGGAAACCTTTTGAAGTGTGCTGCTGCTGATTTGAGC 2690
Db 3177 CACUCUGCAUGAUGAGCGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3236
QY 2691 GCAACTCCACTGCTGATTTTCCAGTCTTCCCGCATGTTCTAGTCTGCTGACTAGA 2750
Db 3237 CUUACACAGUCCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3296
QY 2751 CACACAAAGAGTTCAAATATTACACCGTAGTGTGTAGTCTTTTGTAGTACAGATAATTAGT 2810
Db 3297 CACACCUUGUCUCAAAGUACUACUCUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3356
QY 2811 GATTTGTTCTTTTAACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2870
Db 3357 GAUCUAGAGAAACUUAUGCUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3416

Db 4077 GGCCTGUGUUAUGAGGCUUAUCAGGCAUUAUCUGGACAGUGUUAUCGAGAGAUUU 4136
Qy 3588 CTTTCTTTCTTACTAGGAAACTCCAGAAACAGATTCAAGAAATTTTCTCGGATCTCGACTCG 3647
Db 4137 UGUUUUUAACAAGAAGACACACGCGGAGAUUGAGGAUUUCUUCGGAGAUUCGACAGU 4196
Qy 3648 CACGTTCTCTATGATGTGTAGAACTGGATATTTCTTAAGTATGATAGTCAAGAACGAG 3707
Db 4197 CAUGGCGGAGUAGUUCUGGAGGUGUAUUAUCAAUAUACGACAAUUCUCAAUAUGAA 4256
Qy 3708 TTTCTATGTGCTGTAGATGATGAATATGGAAGATTTGGTCTCAATGATTTTGGCC 3767
Db 4257 UUCACUGUGGAGUAGUUAUCAGAGUUCUGGCGGAAGAUUGGUGUUUAAGACUUCUUGGA 4316
Qy 3768 GAAGTGTGGAACAAGGCGACAGAAACAACTTTTCAAGGATTAACATTTCTGCTGAATCAAG 3827
Db 4317 GAAGUUGGAAACAAGGCAUAGAAGACCACTTCAAGGAUUAUACCGCAGGAUUAAGA 4376
Qy 3828 ACATGTCTGTGTATCAAAAGGAAACGGGTGATGTGACTTCTTCAATCGGCAATCTGTT 3887
Db 4377 ACUGCAUCUGGUUAUCAAAGAAAGAGCGGGACGUCACGACGUUCAUUGGAAACACUGUG 4436
Qy 3888 ATAAATAGCAGCTTCTGTTGGTTCATGTTACCGATGGAAGAAAGTCAATAAGGTGCTTTT 3947
Db 4437 AUCAUUGCGUAGUUGUUGCCUGCAUGUUCGAGGGAAGAAUUAUCAAAGGAGCCUU 4496
Qy 3948 TGTGAGAGAGATTCCGTTTGTATTTTCCAAAGGGTTTGGATTTCCCTGACATTCAGTCA 4007
Db 4497 UCGGUGAGUAGUUGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4556
Qy 4008 TGTGCTTAATCTCATGTGGAATTTTGGGCGCAACTGTATAGAAAGAGTACGTTACTTT 4067
Db 4557 UCCGCGAAUUAUUGGAAUUAUUAAGCAAAACUCUUAUUAUUAUUAUUAUUAUUAUUAU 4616
Qy 4068 TGTGTTAGATACATCATACATGATAGAGGAGCAATAGTATGATGATCTTCTTGAAG 4127
Db 4617 UGCGGAAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4676
Qy 4128 TTGATCTCAAACTTCGGGCAAAACATATCAAGGATTTATGATCATCTTGAAGATTAGG 4187
Db 4677 UGAUUCUGGAAUUAUUGGUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4736
Qy 4188 GTGCTCTTTGCGATGTGCTTCTGCTCGGAAACTGGTCTTAGGCTTTTCGCGAGCTG 4247
Db 4737 AGGUCUUAUUGAGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUG 4793
Qy 4248 AACGAGCTATCAAGAGGTTCTATAAACCGGATGATGTTGCTGTTGTTTAAATGTT 4307
Db 4794 GACGACGUGUUAUGGAGGUGUUAUUAAGACCGCCCGUUGUUGUUGUUGUUGUUGUUGU 4853
Qy 4308 GTTAAACAAATTTTGTGATAAATTTTATTTAGAACTTTGTTTAAATGCTGTTAG 4367
Db 4854 CUGGUGAAGUUAUUGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4913
Qy 4368 TCTCAGAGATCTGTCAAAATTAAGCAGTTCAITGATCTTTTCAAAACAGATGAGATACT 4427
Db 4914 UGUUAAGGAAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4973
Qy 4428 TCCGCAATTCATGATCAAGTCAAGTGTGTTAGATATCGACTGTGGAAGAATTTATGCG 4487
Db 4974 ACCGUGGUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5033
Qy 4488 TGTTAAGATGATGATCTTCTGATGATGATTTTAAAGGTTGTTAGTTAGTAAAGAA 4547
Db 5034 UCAUGAAGUAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5093
Qy 4548 AGGATGTGTGCTAGCTGATTTGTTAGTGTCTGGGAGTGAATCTCCCGATTAATG 4607
Db 5094 UGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5153
Qy 4608 CCGTGTGTGTGCTGATGTTTGTATGATGATGATGATGATGATGATGATGATGATGATG 4667
Db 5154 CAGAGGAGGUGUAGCGUGUGUGUGUGGACAAAGGAAGGAAGGAGGAGGAGGAGGAGG 5213

Qy 4668 GCTGGTGGTATCAAGCCCTGCTTGCACAAAGAAATTTTCTTTTAACTAATCCCTAA 4727
Db 5214 UCUCGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5273
Qy 4728 TTATTTCAATAACATCGGAGTGTGAGAACCCGCTGGCAAGTGTGTAGTGAATATCAA 4787
Db 5274 UUAUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5333
Qy 4788 AGGAGTGGCTATGGAAGAGGATAGTCTCTTTATCTTTTGGAGTTCGTTTCAATTTGTG 4847
Db 5334 AAUUGGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5393
Qy 4848 AGTACATATAAATAATGTAAGAAAGTTTGAAGGAACTATTTTGAAGTGTGACAGCG 4907
Db 5394 UGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5453
Qy 4908 CTCGCAATTTGACTCACTGAAAGGTTGTTTGAAGGTTTCTGTTGATGAAGTCAATGCG 4967
Db 5454 AGGCGCCCAUGGAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5513
Qy 4968 TGTGA 4972
Db 5514 GAUCA 5518

RESULT 4

US-09-962-527-1
Sequence 1, Application US/09962527
Patent No. 6740740

GENERAL INFORMATION:

APPLICANT: GARGER, STEPHEN
HOLTZ, R. BARRY
MCCULLOCH, MICHAEL
TURPEN, THOMAS

TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
FROM PLANT SOURCES

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N.W.
CITY: Washington
STATE: DC

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/962,527

FILING DATE: 24-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/037,751

FILING DATE: 10-march-1998

ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P

REGISTRATION NUMBER: 25,277

REFERENCE/DOCKET NUMBER: 00801.0140.999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-463-8109

TELEFAX: 650-463-8400

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 6395 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: Genomic RNA

[illegible]


```
Db 4794 GACAGCGUGAUGGGAGGUCAUAGACCCGCCCCAGGUGUGUUUUUAUAAAGU 4853
Qy 4308 GTTAACAAATTTTGTGTGATAAATTTTATTAGAACTTTGTTTTAAATGGCTGTAG 4367
Db 4854 CUGGAGAGUAUUGUCUGAUAAGUUCUUUUUAGAGUUGUUUAUAGAUUGGCUUAGU 4913
Qy 4368 TCTCAGAGATCTGTCTCAAAATAGCGAGTTCATTTGATCTTTTCGAAAACAGGATGACT 4427
Db 4914 UGUUAAAGGAAGAGUAUACAUGAGUUUAUACCGUGUCAAAAUUAGGAGAGAUUU 4973
Qy 4428 TCCGGCATTCATGACTAAGGTCAAGAGTGTAGAAATATCGACTGTGACAAAGATTATGGC 4487
Db 4974 ACCGUGAUGUACCCUGUAAGAGUUGUUGUUCNAAGUUGAUAUAAUUAUGGU 5033
Qy 4488 TGTTAAGAATGATAGTCTTTCTGATGTAGATTTACTTTAAAGGTGTTAAGTTAGTAAGAA 4547
Db 5034 UCAUGAGAUGAGUCAUUGUCAGAGGUGAACCUUUAUAGGAGUUAAGCUUAUGAUAG 5093
Qy 4548 AGGTATGTGTCTAGTGTATTTGGTAGTGTCTGGGGAGTGGAAATCTCCCGGATACTG 4607
Db 5094 UGGAUACGUCUGUUUAGCCGUGUGUGUCACCGGCGAGUGGAAACUUGCCUGACAUAUG 5153
Qy 4608 CCGTGTGTGTCTCAGTGTGTGTATTTAGATAAGAGAAATGAAAGGAGTAAGGAAGCAAC 4667
Db 5154 CAGAGGAGUGUGAGCGUGUGUGUGUGGACAAAGGAUGGAAGACCGACGAGGCCAC 5213
Qy 4668 GCTGGTGCCTATCACGCCCTGCTTGCAAAAAGAAATTTTCTTTAAAGCTAATCCCTAA 4727
Db 5214 UCUCGGAUUCUUAUACAGCAGCAGCUGCAAGAAAGAUUUCAGUUCAGGUGUCCAA 5273
Qy 4728 TTATTCATTAACATCCGAGGATGCTGAGAGCACCCGTGGCAAGTGTGTAGTGAATACAA 4787
Db 5274 UUAUGCUAUAACCAACCCAGCAGCGGAUAGAAACGUCUGGCAAGUUUUAUGTUAUUAUG 5333
Qy 4788 AGGATGCTGTATGAAGAGGATACTGCTCTTTATCTTTGAGTTCGTTTCAATTTCTGT 4847
Db 5334 AAUGUGAAGUUGUCAGCGGUGUUGUCUCCUUCUUGUGUUGUGUGUGUGUGUUAU 5393
Qy 4848 AGTACATAAAATTAATGTAGAAAAGGTTTGGAGGAACGTTATTTTGAGTGTGACAGCGG 4907
Db 5394 UGUUUAUAGAAUUAUAAUUAUUAUAGUUGUUGAGAGAGAGAUUAACAAACGUGAGAGCG 5453
Qy 4908 CTCGCCAATTAACCTACTGAAAGGTTTGTGAGAGTTCGTGATGAAGTACCAATGGC 4967
Db 5454 AGGCCCAUGGAACUACAGAGAAGUGUGUGUUGAGUGUUAUGGAUGUCCCUAUGUC 5513
Qy 4968 TGTCGA 4972
Db 5514 GAUCA 5518
```

```
RESULT 5
US-09-259-741-2
; Sequence 2, Application US/09259741
; Patent No. 603895
; GENERAL INFORMATION:
; APPLICANT: GARGER, STEPHEN
; APPLICANT: HOLTZ, R. BARRY
; APPLICANT: MCULLOCH, MICHAEL
; APPLICANT: TURPEN, THOMAS
; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
; TITLE OF INVENTION: PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES FROM PLANT
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
```

```
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/259,741
; FILING DATE: February 25, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/037,751
; FILING DATE: March 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 00801.0140.US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-463-8100
; TELEFAX: 650-463-8400
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6439 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic RNA
; US-09-259-741-2

Query Match 40.9%; Score 2034.2; DB 3; Length 6439;
Best Local Similarity 44.4%; Pred. No. 0;
Matches 2214; Conservative 957; Mismatches 1793; Indels 21; Gaps 4;

Qy 6 AAGTAAATTCCTGAGTTTCAAGGGAGGCTTTTAAACAGGTATGACAGAGTCCCAACGAA 65
Db 537 AAAACAGUCCCAACUCCAAAGGAAGCAUUAUGACAGAUACGAGAAUUCUGAAGAC 596
Qy 66 GTCTGCTGCTCTAAAACCTTTTCAGGATTGTTCGAATACATCCGCCAGAGATAGTGTAGA 125
Db 597 GCUGUCUGUCACAAUACUUCUCCAGCAAAUGCGCAUUCAGCCGAUGCAUACAGGCGA 656
Qy 126 AGATACGCTGTGCTGTCACAGTGTGTATGATATTCCTGTGATGAGTTTGGAGCTGCG 185
Db 657 GUGUAUGCCAUUGGCGUACACAGCAUAUUAUGACAUACACCCGAGUAGUUGGGCGCA 716
Qy 186 TTAATATCTAAGAAATATACATGATGATGATGATGATGATGATGATGATGATGATGAT 245
Db 717 CUCUUGAGGAAAAAUGUCCAUACGUGUUGCGGCUUUCACUUCUCCGAGAACUGCUU 776
Qy 246 CTAGACACGAGCGAGGTTACGCTTAATGAATAGGCGCAACTTTTCAAAAGAGAGAGTGAT 305
Db 777 CUUGAAGAUUACUACGUAUUUGGAGCAAAUACGCGUGUUUUUUCGCGGAGUAGAGAC 836
Qy 306 GATGTTTCTTTTCTTTTCTGCTGATGAAAGTACTTTTAAATTTATAGTCAATAATACAAAAT 365
Db 837 AAGUUGACCUUUCUUUUGCAUCAGAGAGUACUUAUUAUUAUUGCAUUAUUAUUAU 896
Qy 366 ATCTGCAATATAGTATGATTAATCTTACTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 425
Db 897 AUUUUAAGUAUGUGUGCAAAACUUAUCUCCGCGCCUUAUUAUUAUUAUUAUUAUUAUUA 956
Qy 426 GAATTTTCTACTAGGTTTAATCTTGTGTTTGTAAATTTTACCAAGTAGATACCTAT 485
Db 957 GAGUUUUUAGUCCAGAGUUUAUACUUGUUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1016
Qy 486 ATTCTGTACAGAGTGTGTAGCAAGTGTGATAGTGTGATAGTGTGATAGTGTGATAGTGTGAT 545
Db 1017 CUUUUUAACAAAGGUGUGGCCCAUAAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1076
Qy 546 GAAGACGCTTTGCTTACAGAAAAACCTTGGCCATGTTTCAACTGAAAGAGCAATCTTT 605
Db 1077 GAAGACGCAUGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1136
Qy 606 AGAGACACGCTTCGGTTAACTTTTGTGTTCCCTTAAGATGAAGGACATGGTGTAGTACCG 665
```


Qy	2811	GATTTGTCTTTTAAGCTCCTTCTTTTAAATGTATATGTAGAGCAGGTAGTAGA	2870
Db	3357	GAUCUAGAGAAA CUUAGCUCGUA CUUGUAGAUUAAGGUCGAGCAACACAA	3416
Qy	2871	TAGCAATTACAGATGGATCAGTGTTCAAAGGTCATAATCTCTTTTGGGCAACACCTAAA	2930
Db	3417	UAGCAAUUACAGAUUGUACUCGGUUGCAAAAGUUCCAUAUUUUUGUGCGCGCCNAAG	3476
Qy	2931	TCAGGAGACTTTCAGATCTACAGTCTTATTTACGATATATGCTCCCTCTGTAATAGTACT	2990
Db	3477	ACUGUGAUUUUCUGAUUACGAGUUUUA CUUAGUAAGUGUCCUCCAGGCAACAGCACC	3536
Qy	2991	ATACTTAACAAGTATGATGCTGTTTACCATGAGGTTACGTGATAATAGCTTTTAATGTGAAG	3050
Db	3537	AUGAUGAAUAUUUGAUGCUGUUAUCAUGAGGUUGACUGACAUUUAUGAAUGUCAAA	3596
Qy	3051	GATTGTGCTCTTGATTTTTCCAAAGATATTTCCGATGCGAAAGGAGGTGAACCATGTCTA	3110
Db	3597	GAUUGCAUUAUGGAUUGUCUUAAGUCUGUGUGCGCCUAAGGAUCAAUCAAACACCAUA	3656
Qy	3111	GAGCCAGTTTTCGTACTCGCGCGCGGAACCGCAAGGCGCTCGAGACTACTCGAAAATCTG	3170
Db	3657	AUACCUAUGUACGAA CGGCGGCAGAAUAGCCAGCCAGACUGGACUUAUGGAAAUUUA	3716
Qy	3171	GTTGCAATGATTAAGAATAATTTCAACGCACACGACCTGACGGGACGATTGACATTTGAG	3230
Db	3717	GUGCGAUGAUUAAAAGAAA CUUUAACGCAACCCGAGUUGUCUGCAUCAUUGAAUUGAA	3776
Qy	3231	AGCACCCACTGTTGTAGTAGATAAGCTTTTGTATAGCTATTTTATTTAAAAGAAAAA	3290
Db	3777	AUAUCGACUUCUUGGUUGAUGAUAAGUUUUUGAUGUUUUUGUUUAAAAGAAAAAAGA	3836
Qy	3291	TACACAAAAAATATGTCTGAGTGATGACGAAGGATTCATATGATGATGATGTTTGGAAAA	3350
Db	3837	AAACCAAAUAAAAGUUUUCUUGUUCAGUAGAGAGUCUCUCAUAGUUGUAGAAAAG	3896
Qy	3351	AGGAAAGAAGTACTATTGGAGCACTTGCGCTTAACTACAATTTTACAGATCTGCGGCCATC	3410
Db	3897	CAGAAACAGGUAAACAUAAGCGCAGUCGCGCAGAUUUAUUUUGUGGAUUGCCAGCAGUU	3956
Qy	3411	GATCAGTACAGACATGATCAAGGCTCAACCAAAAACAGAAATTTGGACCTTTCAATTCAG	3470
Db	3957	GAUCGAGACAGACACAUGAUUAUAGCAACACCCAAACAAAGUUGGACAUUCAUCCAA	4016
Qy	3471	AATGAATACCTGCTCTGC AAAACAATTTGCTACCATTTCGAAGCAGATCAACGGTATTTTG	3530
Db	4017	ACGGAGUACCCGGCUUUGCAGACGAUUGUUAUCCAUUCAA AAAAGAUCAUAGCAUAUUC	4076
Qy	3531	GCGGGTTTCT---CAGAGCTTACAAGTTGTGCTCGAGGCAUATTGATTTCTAAGAAGTTT	3587
Db	4077	GGCCGUGUUGUUGAGAGCUUACUAGGCAAUUACUGGACAGUGUGUAGUCGACGAGAUU	4136
Qy	3588	CTTTTCTTTACTAGGAAAATCCACAGAACAGATTCACAGAAATTTTTCTCGGATCTCGACTCG	3647
Db	4137	UUGUUUUCAACAAGAAAGACACACAGCGAGAUUGAGGAUUUUUCUGGAGAUUCUCCACAGU	4196
Qy	3648	CAGTTCCTATGGATGTGTTAGAACTCGGATAATTTCTAAGTATGATAAGTCAACAGAACGAG	3707
Db	4197	CAUGUGCCGAUGAUGUUGGAGCTUGGAUAUAUCAAUUAUCAAUUAUUAUUAUUAUUAUUA	4256
Qy	3708	TTTTATTTGCTGTAGAGTATGAATAATGGAAGATTGGGTCTCAATGAGTTTTTGGCC	3767
Db	4257	UUCACUUGUGCAGUAGAAUACGAGAUUCUGGCGAAGAUUGGGUUUUGAAGACUUCUUGGGA	4316
Qy	3768	GAACTGTGGAACCAAGGCGACAGGAAAACAACTTTTGAAGGATTACATTTGCTGGAATCAAG	3827
Db	4317	GAGUUUGAAACAAAGGCAUAGAAAGNCCACCCUCAAGGAUUUAUUAUUAUUAUUAUUAUUA	4376
Qy	3828	ACATGTCTGTGGTATCAAGAGAAAGCGGTGATGTGACTATTTTCATCGGCAATACTGTT	3887
Db	4377	ACUUGCAUCUGGUUAUCAAAGAAAGAGGGGAGCGUCACGAGUUUAUUGGAAACACUUGU	4436

Qy	3988	ATAAATGACACTGCTTGGGTTCAATGTTACCGATGGAAGAGTCATAAAGAGTGCTTTT	3994
Db	4437	AUCAUUGCUGAUUUGGCGCUGAUGCUUCCGAUGAGAGAAAAAUAUCAAAAGAGGCCUU	4496
Qy	3948	TGTGGAGACCAATTCGTTTGTATTTTCCAAAAGGTTTGGATTTCCCTGCACATTTCAGTCA	4007
Db	4497	UGCGGUGACCAUAGUCUGUGUACUUUCCAAAGGGUUGUGAGUUUCCGGAUGUGCAACAC	4556
Qy	4008	TGTGCTAATCTCATGTGGAAATTTTGAGGCCCAAACTGTATAGAAAAGAGTACGGTTACTTT	4067
Db	4557	UCCGCGAUCUUAUGUGGAUUUUGAAGCAAAACUGUUAUAAAAACAGUAUGGAUACUUU	4616
Qy	4068	TGTGGTAGATACATCATACACCAATGATPAAGGGAGCAATAGTGTATTATGATCTTTGAAG	4127
Db	4617	UGCGGAAGAUUGUAUAUCAACGACAGAGGAUGCAUUGUGUAUUAUGAUCGAAUCCCUAAAG	4676
Qy	4128	TTGATCTCRAAACTTGGGGCAAAACATATCAAGGATATGATCACITTAGAAGAGTTAAGG	4187
Db	4677	UUGAUCUCGAAAACUUGGUGCAAAACAUCAAAGAUUGGGAAACUUGGAGGAGUUCAGA	4736
Qy	4188	GTGTGTTGTGCGATGTTGCTGTTCTCGTCGGAACATGGTGCTTAGTGCTTTCGCGACGTG	4247
Db	4737	AGGUCUUCUUGAUGUUGUGUUCUUUGU---GAAACAUAUGUGGUAUUAACACAGUUG	4793
Qy	4248	AACGCACTATCAAGGAGGTTTCATAAAACCGCATGATGGTTGCTTTGCTTTAAATGTT	4307
Db	4794	GACGACGUCUGAUGGAGGAGUUAUAAGACGCGCCUCCAGGUUGUUUAUAAAAAGU	4853
Qy	4308	GTTAACAAAATTTTGTGTGATAAATTTTATTTATTTAGAACTTTGTTTTAAATGCTGTTAG	4367
Db	4854	CUGGUGAAGAUUUGUCUGAUAAGUUAUUGUUUAGAGUUUUUUAUGAUGGUCUCUAGU,	4913
Qy	4368	TCTCAGAGATACTGTCAAAATTAGCAGGTTTCATTGATCTTTTCGAAAACAGGATCAGACT	4427
Db	4914	UGUUAAGGAAAAGAGUAUAUCAUAAGUUUUCGACCUUGCAAAAUGGAGAGAUCUU	4973
Qy	4428	TCCGCGCAATTCATGACTAAGGTCGAAGTGTTAGAAATATCGACTGTGACCAAGATTATGCG	4487
Db	4974	ACCGUGCAUGUUUACCCUCUGAAGAGAGUUAUGUGUUCGAAAGUUAUAAAAUUAUGU	5033
Qy	4488	TGTTAAGAATGATAGTCTTTCTGATGTAGATTACTTAAAGGTTGTTAAGTTAGTTAAGAA	4547
Db	5034	UCAUGAGAUGAGUACAUGUCAGAGGUGAACCUUCUUAAAAGSAGUUAAGCUUAUGAUG	5093
Qy	4548	AGGATGTGTGCTAGCTGATTTGTGTAGTGCTGTGGGAGTGGAACTCTCCCGGATACTG	4607
Db	5094	UGGAUACGUCUGUUUACCCGUGUUGGUCUCACGGCGAGUGGAAACUUGCCUGACAUAUG	5153
Qy	4608	CCGTGCTGTGTGAGTCTTTTGTATTGTAGATAAGAGAAATGAAAAGGAGTAAAGAAACAAC	4667
Db	5154	CAGAGGAGGUGUGAGCGUGUGUCUGUGGACAAAAGGAUGAAAGCCGACGAGGCCAC	5213
Qy	4668	GCTGGGTGCGTATACGCGCCCTGCTGTGCAAAAAGAAATTTTCTTTTAAGCTAATCCCTAA	4727
Db	5214	UCUCGAUCUUUAUCAACAGCAGCUGCAAAAGAAAAGAUUUCAGUUAAGGUCUGUCCCAA	5273
Qy	4728	TTATTCAATTAACATCCGAGGATGCTGAGAGCACCCGTGGCAAGTGTTAGTGAATATCAA	4787
Db	5274	UUAUGCUAAACCAACCCAGGACGCAUGAAAAAACGUCUGCAAGUUUUUAUUAUUAUG	5333
Qy	4788	AGGAGTGGCTATGGAAGAAGATCTGCTCTTTATCTTTGGAGTTCGTTTCAATTTGTGT	4847
Db	5334	AAUUGAAGAUGUCACGCGGUUUCUGCCGUUCUCUGGAGUUGUGUCGGUGUGUUAU	5393
Qy	4848	AGTACATAAAAAATAATGTAGAAAAGGTTTGAGGGAAACGTATTTTGTAGTGTGACAGACGG	4907
Db	5394	UGUUUAUAGAAAUAUAUAAAAUUAUGUUUGAGAGAGAAGAUUAACAACCGUGAGACGG	5453
Qy	4908	CTCGCCAAATGCACTCACTGAAAGGTTGTGTAGGAGTTCGTGATGAAGTACCAATGGC	4967
Db	5454	AGGCGCCCAUGGAACUUAACAAGAAAGUCUGUUGAUGUUAUGGAAUGAUGCUUUAUGUC	5513
Qy	4968	TGTGA 4972	

Db 5514 GAUCA 5518

RESULT 6
US-09-037-751-2
; Sequence 2, Application US/09037751
; Patent No. 6037456
; GENERAL INFORMATION:
; APPLICANT: GARGER, STEPHEN
; APPLICANT: HOLTZ, R. BARRY
; APPLICANT: MCCULLOCH, MICHAEL
; APPLICANT: TURPEN, THOMAS
; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
; TITLE OF INVENTION: PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
; TITLE OF INVENTION: FROM PLANT SOURCES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,751
; FILING DATE: 10-MAR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 00801.0140.999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-463-8109
; TELEFAX: 650-463-8400
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6439 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic RNA
; US-09-037-751-2

Query Match 40.9%; Score 2034.2; DB 3; Length 6439;
Best Local Similarity 44.4%; Pred. No. 0;
Matches 2214; Conservative 957; Mismatches 1793; Indels 21; Gaps 4;

QY 6 AAGGTAATTCCTGAGTTTCAAGGGAGGCTTTTAAACAGGTATGCAGAGCTCCCAACGAA 65
DB 537 AAAACAGUCCCCAAUUCUCAAAGGAAGCAUUGACAGAUACGCGCAGAAAUUCUGAAGAC 596
QY 66 GTCTGCTCTTAAACTTTTCAGGATTTCGAAATACATCCCGCAGAGATAGTGTAGA 125
DB 597 GUGUGUGUCACAAUUCUUCAGACAUUGCGGACAUCCGCGGAGCAUUCAGGACGA 656
QY 126 AGATACGCTGTGCTCTGCACAGTTTGTATGATATTCCTGTGATGAGTTTGGAGCTGG 185
DB 657 GUGUAGCCAUUGCGGCUACACAGCAUUAUGACAUACACGACGAGUAGUUGGGGGGCA 716
QY 186 TTAATATCTAAGAAATATATGATGATGATGATGATGATGATGATGATGATGATGAT 245
DB 717 CUUUGAGGAGAAAUGUCCAUUGCGUUGCGGUUCCAUUCUCCGAGAAACUGCUU 776

QY 246 CTAGACCAGACGGAGGTTACGCTTAAATGAATAAGCGCAACTTTTCAAAAGAGAAGGTGAT 305
DB 777 CUUGAAGAUCAUACGUAUUGGACGAAAUCAACGCGUUGUUUUCGCGGAGUAGAC 836
QY 306 GATGTTCTTTTCTTTTCTGCTGATGAAGTACTTTTAAATTAATAGTATAGTATACAAAAT 365
DB 837 AAGUUGACCUUUUUUUUGCAUGACAGAGUACUCUUUAAUUAUUGUUGUUGUUGUUGUUG 896
QY 366 ATCTTGCAATTATAGTATGTTTAAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 425
DB 897 AUUCUUAAGUUGUGUACAAACUUCUUCGCGGCUUUAUAGAGAGUUGUUGUUGUUGUUG 956
QY 426 GAAATTTTGTACCTAGGTTTAACTTTGTTTGTAAATTTTAAATTTTAAATTTTAAATTT 485
DB 957 GAGUUUUGUACCCAGAGUUAUACCGUUGUUUUGUUAAGUUUUGUUAAGUUUUGUUAAG 1016
QY 486 ATTCTGTACAGAGTGTGTAGCAAGTGGTGTGTAGTGTGTGTGTGTGTGTGTGTGTGT 545
DB 1017 CUUUUGUACAAAGGUGUGCGCCAUAAAGUUGUAGUAGGAGCGUUUUUUAUUCUGAAUG 1076
QY 546 GAAGACGCTTTTGTCTTACAGAAAACCTTGGCCATGTTTCAACACTTGAAGAGCAATCTTT 605
DB 1077 GAAGACGCGUUGCAUUAACAAAGAGACUCUUGCAUUGUGCAACAGCAGAGAUUCUUCU 1136
QY 606 AGAGACGCGTTTGGTTTAACTTTTGGTTTCCCTAAGATGAAGGACATGGTGTATGATCG 665
DB 1137 GAGGAUUCAUCAUGACUAAUUAUCUGUUUCCAAAUGAGGGAUUGUUGUUGUUGUUG 1196
QY 666 CTGTTTGGGTTTCTTATTTACAGAAAAGATGCAAGGAGTGAGGTGATGTTTAAATCGT 725
DB 1197 UUAUUCGACAUUCUUGGAGACUAGUAAAGAGGCGCGCAAGAAAGUUGUUGUUGUUG 1256
QY 726 GACTTCGTTTACACAGTCTTAAATCATATCAGAAATATCAAGCCAAAGCGTTTAACTTAC 785
DB 1257 GAUUCUGUUGUACAGUGCUUAACCAUUCGAAUACCAAGCCGCGGAGGCUUUAUAC 1316
QY 786 CAGAACGATTTATCTTCTGAGGTCATATAGATCCCGGTGTATATCAATGGTGTACT 845
DB 1317 GCAAAUGUUUUGUCCUUGGAGUUGGACAAAUUUUUAUUCGAGGUAUUAUUAUUAUUA 1376
QY 846 GCTAGGTCGATGGGATGATGAAGCAATTTCTCAACCTTCTCTCAATGATTTCTTC 905
DB 1377 GCGAGGCGGAAUGGAGUUGGACAAAUUUUUAUUCUUGUUGUUGUUGUUGUUGUUG 1436
QY 906 TTGCAGACTAAGTGGCTTCAAGACGATATAGTAATGGGAAAGTTTCGGTCTCTG 965
DB 1437 CUGCAUACUAGCUGUUGCGUUAUAAAGUAGCUUACUAGUAGCAUUAUAGUUGUUG 1496
QY 966 GATAAGACCATTTCTGAACTTTATTTGGGATGAGTGGGCAAAATTTTTGGAAACGTTTTC 1025
DB 1497 UCGAAAACGGUGUGCCAGCAUGUGGAGUAGAUUUCGUGCGGUUGGAAACGCAU 1556
QY 1026 CCCACTATCAAGAGAGATTTGGTGAAGGAAATTTCTGGATGTAAGTGAAGTCTCTG 1085
DB 1557 CCUCUUGGAAAGAGAGACUCUUGAAGCAGGAAACUUAUCAGAGUGGCGGCGGCAUUA 1616
QY 1086 AAGATCAAGATCCAGATCTGTATCTCATGGAAGACAGAGTCTGTAGCTGAATACACC 1145
DB 1617 GAGUACAGGUGUCCUAGUUAUUGUAGCUUCCAGCAGACAGAUUAGUAGUAGUAGUAG 1676
QY 1146 AAGTCTGAGGAGTTTACCGCATCTAGATATCAAGAAAGGCTTTAGAAAGAGCTGAG 1205
DB 1677 GCUCUUGGACAUUGCGUUGUAGUAGAUUAGGAAAGAGAGAAAGAAAGAGAGUAG 1736
QY 1206 THAGAGCGGTTATCAGAAATTTATCTTAAAGGTTGCTGATTAATTTTCAATATCGGA 1265
DB 1737 UACAAGUACAUUUCAGAUUUCGUGUUAAGGAGUUGUAGUAGUAGUAGUAGUAGUAG 1796
QY 1266 TTTCAAGACATGTGCAAGCTTTTATGTTTCTGTGTGTGTGTGTGTGTGTGTGTGT 1325
DB 1797 UUUUCCGAGUUGGCAUUCUUGGAAUUGGAAUUGGAAUUGGAAUUGGAAUUGGAAUUG 1856
QY 1326 GCAGTGGCGGAGAAATAGAGGCGGTTTAACTCTTCTTTTGTATAGCCAAACCGAGGA 1385

		STRANDEDNESS: single	
		TOPOLOGY: unknown	
		MOLECULE TYPE: Genomic RNA	
		SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
		US-09-466-422-2	
		Query Match 40.9%; Score 2034.2; DB 3; Length 6439;	
		Best Local Similarity 44.4%; Pred. No. 0;	
		Matches 2214; Conservative 957; Mismatches 1793; Indels 21; Gaps 4;	
Qy	6	AAGTAAATTCCTGAGTTTCAAGGAGGCTTTTAAACAGGTATGCAGAGCTCCCAACGAA	65
Db	537	AAACAGAGCCCAACUCCAAAGAGAGCAUUGACAGAUACGCGAAGAUUCCUGAAGAC	596
Qy	66	GTCTGCTGCTCTAAACCTTTTTCAGGATTGTGGAATACATCCGCCAGAGAAATAGTGTAGA	125
Db	597	GCUGUCUGACAAUACUUCACAGCAUUGCGACAGCGCGAUCAGGCGAGA	656
Qy	126	AGATACGCTGTGCTGACAGCTTTGTATGATATTCCTGTGATGATGTTTGGAGCTGCG	185
Db	657	GUGUAGCCAUUGCGUACACAGCAUAUAGACAUAACCCAGCGAGUAGUUGCGGCGCA	716
Qy	186	TTAATATCTAAGATATACATGTATGTATGCTATGCTTCCATTTTGGCAGAGCAATTATTA	245
Db	717	CUCUUGAGGAAAAUGUCCAUACGUGUAGCCGCUUCCUUCUCCGAGAACCCGCUU	776
Qy	246	CTAGACACAGCGAGGTTTACCTTTAAATGAATAGCGCACTTTTCAAAAGAGAGGTGAT	305
Db	777	CUUGAAGUUAUACUGCUAAUUGGACGAUAUACCGGUGUUUUCGCGGAGGAGAC	836
Qy	306	GATGTTTCTTTTCTTGTGATGAAAGTACTTTTAAATATATAGTCAATAATACAAAT	365
Db	837	AAGUUGACCUUUCUUGCAUCAGAGAGUACUCUUAUUAUUGCAUUAUUCUUAU	896
Qy	366	ATCTTGATATGTAGTTAAATCTTACTTTCTCTCTCTAGTAGAATAGTTACTTTAAG	425
Db	897	AUUCUUAAGUUGUGUAAAAACUUAUUCGCGCCUUAUAGAGAGGUGUUUAUAGUAG	956
Qy	426	GAAATTTTGTAGTCACTAGGTTTAACTTTGTTTGTAAATTTTACAAAGTAGTACCTAT	485
Db	957	GAGUUUUAUGACACAGAUUAUACUGGUUUUUAAGUUUUAUAGAUUAUUAUUAU	1016
Qy	486	ATTCTGTACAAGAGTTGTAGCAAGTAGGTTGTATGATGATCTATGAGGCGATG	545
Db	1017	CUUUGUACAAAGGUGUGGCCCAUAAAAGUGUAGUAGAGGAGCAGUUUAUACUGCAA	1076
Qy	546	GAAGACGCTTTGCTTACAAGAAACCTTTGCGCATGTTCAACACTGAAAGAGCAATCTTT	605
Db	1077	GAAGACGAGGCAUUAACAAAGAGACUUCUUGCAUUGUGCAACGAGAGAAUCCUCCU	1136
Qy	606	AGAGACACGGCTTCGGTTAACTTTTGTTCCTTAAGATGAGGACATGGTGATAGTACCG	665
Db	1137	GAGGAUUAUACUACAGUUAUACUGGUUUCCAAUAGAGGGAUUGGUCAUCGUACCA	1196
Qy	666	CTGTTTGAGGTTCTATTACAGCAAAAGATGACAGAGTAGGTCATTGTTAAATCGT	725
Db	1197	UUAUUGACAUUUCUUGGAGAUAGUAAAGAGGACGCGCAGGAGUAGUUGUCCAAAG	1256
Qy	726	GACTTCGTTTACAGTGTCTTAATCATATCAGACATATCAAGCCAAAGCGTTAACTTAC	785
Db	1257	GAUUGUGUUUAUACAGUGCUUAACCAUUGGAACAUACCGGGAAGGCUUUAUACADAC	1316
Qy	786	CAGAACGTTATTCTTTGCTGAGTCTATAGATCCCGCGTGAATAATCAATGGTGTACT	845
Db	1317	GCAAUUUUUUUGUCCUUGCAUUGCAUUGAGGAGGUAUUAUUAACGUGUGACA	1376
Qy	846	GCTAGGCTGAATGGGATGTAGATAAAGCAATCTTCAACCTTTGTCAATGACTTTCTTC	905
Db	1377	GCGAGGCGGAAUGGAGUGGACAAAUUCUUGUUAUCAAUUCUUGUUGCAUGCUUUAC	1436
Qy	906	TTGACAGTACGCTGCGCTTCAGACGATATAGTAATGGGAAAGTTTCGGTCTTG	965
Db	1437	CUGCAUACUAGGCUUGCCGUUAAGAGUACUUAUCUGUAUAGAUUUAUGUCUGU	1496

Qy	966	GATAAGACCACTTCTGAACCTTATTTGGGATGAGGTGGGCAAAATTTTGTGAAACGTTTTC	1025
Db	1497	UCGAAAAACGGUGUGCCAGCAUGUGUGGAUUAUUCGUGCGUUGGGAACGCAUUU	1556
Qy	1026	CCCACTATCAAGAGAGATTTGGTGACAGGAAATTTCTGATGTAAGTGAAGATGCTCTG	1085
Db	1557	CCUUCGUGAAGAGAGACUCUUGAACAGGAAACUUAUCAGAGUGGCGGCGACGCAUUA	1616
Qy	1086	AAGATCAAGATCCAGATCTGTATGTACATGGAAGACAGGTTTCGTAGCTGAATAACCC	1145
Db	1617	GAGUACAGGGUGGCUAGUUAUUAUGUAGCCUCCACGACAGAUUAGUGACUGAGUACA	1676
Qy	1146	AAGTCTGAGGAGTTACCGCATCTAGATATCAAGAGGACTTTAGAAAGCTTGAGCAATG	1205
Db	1677	GCUCUGUGGACAUUGCGUGUUAUAGGAAGAAUGAAGAAAGAAACGGAAGUGAUG	1736
Qy	1206	TACGACGCTTATCAGAAATTTATCTTAAAGGTCTGTATATTTTCGATATCGCGAAG	1265
Db	1737	UACAAUGCACUUUCAGAUUACGGUGUUAAGGGAGUCUACAAAUUCGAUUGUUAUGUU	1796
Qy	1266	TTCAAAGACATGTGCAAGGCTTTAGATGTTAGTCTCTGATGTGGCAGCACGAGTAATCGTT	1325
Db	1797	UUUUCGAGUAGCCAAUUCUUGGAGUUGACCAUAGACGCGACGCGAAGGUUAUAGUC	1856
Qy	1326	GCACTGCGCGAGAAATAGAGCGGTTTAACTTTTCTTTTGAAGCCAAACGAGAGAAAT	1385
Db	1857	GCGUCAUGACAAUGAGAGCGGUCUGACUCUCACAUUUGAACGACCUACUGAGCGGAU	1916
Qy	1386	GTGCTTAAAGCTCT-----TAAAGCACGCGCTCTGAGCGCGTGTGTATCTTTGAACCG	1439
Db	1917	GUUGCGUAGCUUUAACGAGAUCAAGAGAGGCUUCAGAAAGGUGCAUUGUUAUACCUCA	1976
Qy	1440	ACATCCGACAGGTGAAGCTAAATAAATTTTCTTATTTCTGAGAAAGGAGATTGCCTGTG	1499
Db	1977	AGAGAUUAGAGAAACGUCUAGAGGUGUUCGUGCCAGAGAGAGAUUAUUAUAGU	2036
Qy	1500	TGTGCGAGAAAGTCTGTTTTCAGCAATGTCTTAACTTAGACACACGAGGATTTGGATCCCTC	1559
Db	2037	GGUUCUGGAGAUCAUCGCGAGUCGUCCUUAUUAAGAAACGAGGAGUAGAGUCUUUA	2096
Qy	1560	AACGATTTCCATAGCTTTCGCTGGATGTGTATTACAAGCAAAATGGCATCGGTTGTC	1619
Db	2097	GAGCAUUAUUAUUGGCGAGGAGAUUCUUAUUAUUGAAGAGAGUAGUAGUCCUUAUGUG	2156
Qy	1620	TACACTGGCTCACTCAAAAGTTCAACAAATCAAGAACTATGTGGACAGTTTGGCAGCTTCG	1679
Db	2157	UACACGGUCCGAUUAAGAUUUCAGCAAAUGAAGAAACUUUAUCCGAUAGCCUGUAGCAU	2216
Qy	1680	TTGTCGCGCACTGTATCAAAATCTATGCAAGTCTCTAAAGGATGAAAGTCGGGTATGATCT	1739
Db	2217	CUAUCUGUGCGGUGCGAAUUCUGUACAGUCCUCAAAGUCCUAAAGUACAGCUGCUUUA	2276
Qy	1740	GATTCAGGAGAGAAAGTTGGTGTCTTGGATGTCACTTTGAAAAGTGGCTCCCTCAAACT	1799
Db	2277	GAAACCGCUAAAAGUUGGAGUUGGAGUUGCAUUAAGGAGGUGUUAUUAUCAAACCA	2336
Qy	1800	CGCGCAAAAGCTCATTCATGGGAGTTGTCTCTGATTTACAAGGGGGAATAATGTTTACTGCA	1859
Db	2337	ACGCGCAAGAGUACUAGCUGGGGUGUUGUUAAGAACCCACCGAGGAAGUUAUAGUGCGG	2396
Qy	1860	CTTCTATCTTATGAAGAGATAGAAATGGTGAAGTGTGAGAGCGACTGGAGAGGGTGGTGA	1919
Db	2397	CUUUGGAUUAUAGUAGAGAGGCGGUGUGACAUUGCGAUUGGAGAGAGUAGUGUUU	2456
Qy	1920	TCATCTGATCAATGTTATATTCTGATATTTGCAAGCTCCAAATCTGAGGAAACAAATG	1979
Db	2457	AGUCUGAGUCUGUUGUUAUUCGACAGGCGGAAACUCAGAAACUCUCGCGAGACUCUU	2516
Qy	1980	AGAGACGCTGAAACCCACAGCAACTACTCTGCAAAAGATGTTGTTGGATGGGTCCTCGGT	2039
Db	2517	CGAAACGAGAAACCGCAUGACUAGUAGCGCAAGAGUUGUUAUUGGAGCGAGUUCGCGG	2576


```

Db 4737 AGGUCUCUUUGUGAUGUUUGUUUCGU---GAAACAAUUGUGCGUUAUACACACAGUUG 4793
Qy 4248 AACGACGCTATCAAGGAGTTTATAAAACCGCGATTGATGTTTGGTTTAAATTTGT 4307
Db 4794 GACGACGUGAUGGAGGUUAUAGACCGCCGCCUCCAGGUGUUUGUUUAUAAAGU 4853
Qy 4308 GTTAAACAAATTTTGTGTGATAAATTTTATTAGAACTTTGTTTAAATGGCTGTAG 4367
Db 4854 CUGUGAAGAUUUGUCUGAUAAGUUUUUUAAGAUUUUUUAUAGAGGCGUUGU 4913
Qy 4368 TCTCAGAGACTCTCAAAATTTAGCGAGTTTCATTGATCTTTTCGAAACAGGATGACT 4427
Db 4914 UGUUAAAGGAAGAGUAUUAUGAGUUUUCGACUUGUUAUUAAGGAGAAGU 4973
Qy 4428 TCCGGCATTCATGACTAAGGTCAGAGGTTTGAATATTCGACTGTGGACAAGATTATGGC 4487
Db 4974 ACCGUGAUGUUUACCCUGUAAGAGUGUUUGUUCUCAAAGUUAUAAUUAUGGU 5033
Qy 4488 TGTTAAGATAGTCTTCTGATGTAGATTTACTTTAAAGGTGTTAGTTAGTTAAGAA 4547
Db 5034 UCAUGAGAAUGAGUUGUCAGAGGUGAACCUUUAAGAGGUAAGCUUAUUGAUG 5093
Qy 4548 AGGTATGTGCTTGTAGTCTGATTTGGTAGTCTCTGGGAGTGAATCTCCCGGATACTG 4607
Db 5094 UGGAUACGUCUGUUUAGCGGUUGUGUCACCGGCGAGUGGAACUUGCCUGACAUG 5153
Qy 4608 CCGTGGTGTGTCTGATGTTTGTATTTAGATAAGAAATGAAAGGAGTAAGGAAGCAAC 4667
Db 5154 CAGAGGAGUGAGUGUGUGUGUGGACAAAGGAGUAGGAAAGAGCGGAGGCGCAC 5213
Qy 4668 GCTGGTGTGCTATCAGCGCCCTGCTGTCGAAAGAAATTTTCTTTTAAAGCTAATCCCTAA 4727
Db 5214 UCUGGAUUAUACACACAGCAGCUGCAAGAAAGAAUUAUGUUAAGGUGUCCUCAA 5273
Qy 4728 TTATTCAATAACATCCGAGGATGTGAGAAGCACCCTGGCAAGTGTGTAGTGAATATCAA 4787
Db 5274 UUAUGCUAUAACCCAGGACGCGAUGAANAACGUCUGGCAAGUUUAUUAUUAUG 5333
Qy 4788 AGGAGTGTGTATGGAAGAGGATATGTCCTTTTATCTTTTGGAGTTTCTCAATTTGTT 4847
Db 5334 AAUUGAAGAUUGUCAGCGGUGUUUGUCGCUUUCUGGAGUUUGUGCGGUGUGU 5393
Qy 4848 AGTACATAAATAATGTAAAGAAAGTTTTCAGGGAACGTTATTTTGTGTGACAGCGG 4907
Db 5394 UGUUUAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5453
Qy 4908 CTCGCCAATGAACCTCACTGAAAGGTTTGTGAGGAGTTCTGTGATGAAGTACCAATGGC 4967
Db 5454 AGGGCCCAUGGAACUUAACAGAAAGAGUUGUUGAUGAUGUUAUGGAGUCCUUAUGUC 5513
Qy 4968 TGTGA 4972
Db 5514 GAUCA 5518

```

RESULT 8

```

US-09-962-527-2
; Sequence 2, Application US/09962527
; Patent No. 6740740
; GENERAL INFORMATION:
; APPLICANT: GARGER, STEPHEN
; HOLTZ, R. BARRY
; McCULLOCH, MICHAEL
; TURPEN, THOMAS
; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
; PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
; FROM PLANT SOURCES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue N.W.
; CITY: Washington
; STATE: DC

```

```

; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,527
; FILING DATE: 24-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/037,751
; FILING DATE: 10-march-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 00801.0140.999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-463-8109
; TELEFAX: 650-463-8400
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6439 bases pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-962-527-2

Query Match 40.9%; Score 2034.2; DB 4; Length 6439;
Best Local Similarity 44.4%; Pred. No. 0;
Matches 2214; Conservative 957; Mismatches 1793; Indels 21; Gaps 4;

Qy 6 AAGTAAATCTCTGAGTTTCAAGGAGGCTTTTAAACAGGTATGACAGAGTCTCCCAACGAA 65
Db 537 AAAACAGUCCCAACUCCCAAAGGAAGCAUUAUGAUAACGAGAAUCCUGAGAC 596
Qy 66 GTCTGCTGCTTAAACTTTTCAGGATTGTGCAATACATCCGCCAGAGAAATAGTGGTAGA 125
Db 597 GCUGUCUGACAAUUAUCCAGACAAUUGCGCAUACAGCCGAGUAGUCCGAGCAGAG 656
Qy 126 AGATACGCTGTGCTGACAGATTGTTGATGATTTCTGTGATGATTTTGGAGCTCG 185
Db 657 GUGUAGCCAUUGCGUACACAGCAUAUAGCAUACAGCCGAGUAGUCCGGGCGGCA 716
Qy 186 TTAATATCTAAGATATACATGTTATGTCAGCTTCCATTTTGGCAGAGCATTTATTA 245
Db 717 CUUUGAGGAAAAGUCCCAUACGUGCUUUGCCGUUCCACUUCUCCGAGAACCGUCU 776
Qy 246 CTAGACCAGACGGAGTTACGCTTAATAAGATAGTCTTAATATAGTCAATAACAAAT 305
Db 777 CUUGAAGAUUAUACGUCUUAUUGGACGAAUACACGCGUGUUUUCGCGGAGGAGAC 836
Qy 306 GATGTTCTTTTCTTTGCTGATGAAAGTACTTTAATATAGTCAATAACAAAT 365
Db 837 AAGUUGACCUUUCUUUGCAUACAGAGAGACUCUUAUUAUUGUUAUUAUUAUUAU 896
Qy 366 ATCTTGCATTTAGTAAATCTTACTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 425
Db 897 AUUCUUAAGUUGUGGCAAAACUUAUCCCGCCUUAUUAUUAUUAUUAUUAUUAU 956
Qy 426 GAAATTTTGTGCTAGGTTAATCTTTGTTGTTTAAATTTACAAAGTAGATACCTAT 485
Db 957 GAGUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1016
Qy 486 ATTCTGTACAGAGTGTAGACAGTGGGTGTGATGATGATGATGATGATGATGATGAT 545
Db 1017 CUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1076
Qy 546 GAAGACGCTTTTGTCTTACAGAAAAACCTTGGCCATGTTTCAACATCTGAAGAGCAATCTTT 605

```


Db 5454 AGGGCCCAUGGAACUACAGAGAAGUCGUGAUGAGUUAUGGAAGUCCUUAUGUC 5513
QY 4968 TGTGA 4972
Db 5514 GAUCA 5518

RESULT 9

US-08-687-559-2
; Sequence 2, Application US/08687559
; Patent No. 5955647
; GENERAL INFORMATION:
; APPLICANT: Fitchen, John H.
; APPLICANT: Beachy, Roger N.
; TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS TO
; TITLE OF INVENTION: OVERPRODUCE PEPTIDES AND PROTEINS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,559
; FILING DATE: No. 5955647ember 18, 1996
; CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: PCT/US95/01467
FILING DATE: 03-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: Learn, June M.
REGISTRATION NUMBER: 31,238
REFERENCE/DOCKET NUMBER: 07302/011001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-678-5070

TELEFAX: 619-678-5099

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 6395 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLSCULE TYPE: Genomic DNA

IMMEDIATE SOURCE:

CLONE: TMV

US-08-687-559-2

Query Match 40.8%; Score 2031; DB 2; Length 6395;

Best Local Similarity 63.6%; Pred. No. 0; Mismatches 1795; Indels 21; Gaps 4;
Matches 3169; Conservative 0;

QY 6 AAGGTAATTCCTGAGTTTCAAAGGGAGGCTTTTAAACAGGTATGCAGAAGCTCCCAACGAA 65
Db 537 AAAACAGTCCCAACTTCCAAAAGGAAGCATTTGACAGATACCGAGAAATTCCTGAAGAC 596
QY 66 GTCTGCTGCTTAAACTTTTCAAGGATTTGTGGAATACATCCGCGCAGAGAAATAGTGTAGA 125
Db 597 GCTGTCTGTACAAATACTTTCCAGACAATCGCACATCAGCCGATGCGAGCAATCAGGCAGA 656
QY 126 AGATAGCTGTGCTCTGCACAGTTTGTATGATATTCCTGTGTCATGATTTGGAGCTGCG 185
Db 657 GTGTATGCCATTGCGCTACACAGCATATATGACATACAGCCGATGAGTTTCGGGGCGGCA 716
QY 186 TTAATATCTAAGAAATATACATGATGTATGTCAGCTTCCATTTTGGCAGAAGCATTTATTA 245

Db 717 CTCTTGAGGAAAAATGTCCATACGTGCTATCGCGCTTTCACCTTCTCTGAGAACTGCTT 776
QY 246 CTAGACACAGCGAGGTTACGCTTTAATAAATAGCGCAACTTTCAAAGAGAAAGGTGAT 305
Db 777 CTTGAAGATTATACGTCAATTTTGACGAATCAACGCGTGTGTTTTTCGCGCATGAGAC 836
QY 306 GATGTTCTTTTCTTTGCTGATGAAGTACTTTAAATATTAGTCAATAAATAAATAAT 365
Db 837 AAGTTGACCTTTCTTTTGCAATCAGAGAGTACTCTTAATATTGTCATAGTTATTCTTAAT 896
QY 366 ATCTTGCAATTATGTAGTTAAATCTTCTGCTTCTCTAGTAGAATAAGTTTACTTTAAG 425
Db 897 ATTCTTAAGTATGTGCAAACTTACTTCCGGCTCTAATAGAGAGTTTACATGAAG 956
QY 426 GAATTTTGTAGTCACTAGGTTTAAATCTTGGTTTGTAAATTTAACAAAGTAGATACCTAT 485
Db 957 GAGTTTTTGTAGTCAACAGAGTTAATACCTGGTTTGTAAAGTTTCTAGAATAGATATCTTT 1016
QY 486 ATTCTGTACAAGAGTGTAGACAAGTAGGTTGTAGTGTGATGATGATGATGATGATGATG 545
Db 1017 CTTTTGTACAAAGGTGTGGCCCATAAAGAGTGTAGATAGTGAAGAGTGTATATCTGCAATG 1076
QY 546 GAAGACGCTTTGCTTACAAGAAACCTTTGGCCATGTTCAACACTGAAAGAGCAATCTTT 605
Db 1077 GAAGACGATGCGCATTAACAAAGAGTCTTGCAATGTGCAACAGCGAGAGATCTCTCTT 1136
QY 606 AGAGACAGGCTTCGTTTAACTTTTGGTTCCCTAAGATGAAGGACATGTTAGTATACCG 665
Db 1137 GAGGATTCATCATCAGTCAATTTACTGGTTTCCCAAAATGAGGATATGTCATCGTACCA 1196
QY 666 CTGTTTGTAGGTTCTTATTAACGCAAAAGATGACAAGAGTGAAGTCAATTTGTTAATCGT 725
Db 1197 TTAATTCGACATTTCTTTTGGAGACTAGTAAGAGAGCGCGCAAGAAAGTCTTACTGTCCAAG 1256
QY 726 GACTTCGTTTACACAGTCTTAATCATATCAGAAATATCAAGCAAAAGCGTTTAACTTAC 785
Db 1257 GATTTGCTGTTTACAGTCTTAACACATTCGAAATCGATTCGAGGGTAATCATTAACGGTGTGACA 1316
QY 786 CAGAAAGTATTTATCTTTGCTGGAGTCTATAAGATCCCGCTGATTAATCAATCGTGTACT 845
Db 1317 GCAATGTTTGTCTTTGTGCAATCGATTCGAGGGTAATCATTAACGGTGTGACA 1376
QY 846 GCTAGTCTGAATGGGATGTAGATAAGCAATCTTCAACCTTGTCAATGATCTTCTTTC 905
Db 1377 GCGAGTCCGAATGGGATGTGACAAATCTTTTGTACAACTCTGTCATCTGTCATGACGTTTAC 1436
QY 906 TTGACAGCTAAGCTGCTGCGCTTCAAGACGATATAGTAATCGGAAAGTTTTCGGTCTTG 965
Db 1437 CTGCATACTAAGCTTGGCGTCTTAAAGGATGACTTACTGATTAGCAAGTTTAGTCTCGGT 1496
QY 966 GATAAGACCACTTCTGAACCTTATTTGGGATGAGGTGGGCAAAATTTTTCGAAACGTTTTC 1025
Db 1497 TCGAAAACGGTGTGCCAGATGTGTGGATGAGATTCGCTGCGGTTTTCGGAACGCAATT 1556
QY 1026 CCCACTATCAAGAGAGATTTGTTGAGCAGAGAAAATTTCTGGATGTAGTGAAGTGTCTG 1085
Db 1557 CCTCGTGAAGAGAGAGGCTCTTGAACAGGAACTTATCAGAGTGGCAGCGCAGCATTA 1616
QY 1086 AAGATCAAGATCCAGATCTGTGTACATCGAAGAGCAGGTTCTAGTCTGAATACACC 1145
Db 1617 GAGATCAGGTCCTGATCTATATGTGACCTTCCACGACAGATTTAGTGTAGTGAACAAG 1676
QY 1146 AAGTCTGAGGAGTTACCGCATCTAGATATCAAGAAAGGACTTAGAAGAAAGCTGAGCAATG 1205
Db 1677 GCTCTGTGGACATGCTCGCTTGCATTTAGAGAGAGATGGAAGAAACGGAAGTGAAG 1736
QY 1206 TACGACGCTTATCAGAAATTTATCTTCTTAAGGGTGTGATAATTTTCGATATCGGAAG 1265
Db 1737 TACAATGCACTTTTCAAGGTTATCGGTGTAAAGGAGTCTGACAAATTCGATGTGATGTT 1796
QY 1266 TTCAAAGACATGTGCAAGGCTTTAGATGTTAGTCTGTGATGTCGACGACGATTAATCGTT 1325
Db 1797 TTTTCCAGATGTGCCAATCTTTTGGAAAGTTGACCCCAATGACCGGAGGTTATAGTC 1856

QY	1326	GCAGTGGCCGAGATAGAGCGGTTTAACCTCTTACTTTTGTATGATGACCAACCGAGGAGAT	1385
Db	1857	GGCGTCATGACGAATAGAGCGGCTGACTCTCAATTTGAACGACCTACTGAGCGGAAT	1916
QY	1386	GTGGCTAAGGCTCT-----TAAAGACCGGCTCTGAGGCGGTGATGCTTTGAACCG	1439
Db	1917	GTGGCTAGCTTTACAGGATCMAGAGAGGCTTCAGAGGTGCTTTGGTAGTTACCTCA	1976
QY	1440	ACATCCGAGAGGTGAACGTAATAATTTTCTATTGCTGAGAAAGGAGATTTGCTGTG	1499
Db	1977	AGAGAAGTTGAAGAACCGTCCATGAAGGTTTCGATGGCCAGAGGAGATTAACAATTAGCT	2036
QY	1500	TGTCGAGAAAGTCATGGTTTGACGATCTTAACCTTAGAGCACCAGGAGTTGAGTCCCTC	1559
Db	2037	GGTCTGCTGAGAGTCATCCGAGGTCGCTTATTCTAAGAAACGAGAGATAGAGTCTTTA	2096
QY	1560	AACGATTTCCATAAGGCTTGGGTGATAGTGTGATTACAAAGCAAAATGGCATCGGTTGTC	1619
Db	2097	GAGCAGTTTCATATGGCAACGCGAGATTCGTTAATTCGTAAGCAGATGAGCTCGATTGTG	2156
QY	1620	TACACTGGCTCACTCAAAAGTTCAACAAATGAAGAACTATGTGACAGTTTGGCAGCTTCG	1679
Db	2157	TACAGGCTCCGATTAAAGTTTCAGCAATGAAGAACTTTATCGATAGCTGCTAGCATCA	2216
QY	1680	TTGTCGCCCACTGTATCAAACTATGCAAGTCACTAAGAGTAGAGTCGGGTATGATTC	1739
Db	2217	CTATCTGCTGGGTGTCGAATCTCGTCAAGATCTCTCAAGATACAGCTGCTATTGACCTT	2276
QY	1740	GATTCAGGAGAAAGTTGGTGTGGGATGTCACTTTGAAAGAGTGCTCTCAACCT	1799
Db	2277	GAAACCGTCAAAAGTTTGGAGTCTTGATGTTGCACTAGAGAGTGTGTTAATCAACCA	2336
QY	1800	CGCGCAAAAGTCAITTCATGGGGAGTTGTCCTGGATTACAAGGGGAAATGTTTACTGCA	1859
Db	2337	ACGGCAAGAGTCATGATGGGTGTTGTTGAAACCCACGCGAGAGTATCATGTGSGG	2396
QY	1860	CTTCTATCTTATGAAGAGATAGAAATGCTGACTGAGACGCACTGAGAGAGGTGGCTGTA	1919
Db	2397	CTTTTGGAAATATGATGACAGGGGTGTGGTGACATCGCATGATGGAGAGATGAGCTGTC	2456
QY	1920	TCATCTGATACAAATGATATCTTGATATGCAAGCTCCAAATCTCAGGAAACAATG	1979
Db	2457	AGCTCTGAGTCTGTTGTTTATTCGACATGCGGAACTCAGAACTCTGCGCAGTCTGCTT	2516
QY	1980	AGAGACGTGAACCCACGAACTTCTGCAAGATGGTACTTGTGGATGGGGTCCCTGGT	2039
Db	2517	CGAAACGGAGAACCGCATGTCAGTAGCGCAAGGTTGTTCTTGTGACGGAGTTCCGGGC	2576
QY	2040	TGTGGAAGTACAAAGGAGATTTTGAAGATTTGATCTTGATGAGGATTTGATCTTGGTT	2099
Db	2577	TGTGGGAAACCAAGAAATCTTTCCAGGTTAATTTTGTATGAAGATCTAATTTTAGTA	2636
QY	2100	CCTGMAAACCAAGCTGCTGATGATCAGAGAGGGCTTAATTCATCTGGACTGATAGA	2159
Db	2637	CCTGGGAAGCAAGCCGCGAAATGATCAGAGAGCTGCGAATTTCTCAGGAGTTATTGTG	2696
QY	2160	GCCCAATGGAACAATGTGAGAACGGTAGATTCACTTTCTAATGSCAT-----CCAAAA	2210
Db	2697	GCCAGGAGGACAAGTTTAAACCGTTGATTTCTTTTCATGATGAATTTTGGGAAAGCACA	2756
QY	2211	CCGGATCACAAGAGGCTTTTATGATGAAGGTTGATGCTGCACACCGTTGTGTT	2270
Db	2757	CGCTGTCAAGTTCAGAGGTTTATTCATGATGAAGGTTGATGTTGCACTGTTGTGTT	2816
QY	2271	AACCTCTGCTGCTTATCTCTGTTGCGACATCGCATACATTTACGGAGATACACAGCAG	2330
Db	2817	AATTTTCTTGTGGCATGTCAATTGTGCGAAATTCGATATGTTTACGGAGACACACGAG	2876
QY	2331	ATTCTCTTCAATAACAGATTCAGAAATTTCCGCTATCCCAACATTTTGAAGCTGCAA	2390
Db	2877	ATTCACATACATATAGAGTTTCAGGATTCGCGTACCCCGCCCATTTTGGCCAAATTTGAA	2936

QY	2391	GTGATGAAGTTGAGATGAGGAGGACCACTGAGATGCCAGCTGATGATGATTTTTC	2450
Db	2937	GTTACGAGGTGGAGACACGAGAACTACTCTCGTTGTCCAGCGGATGTACACATAT	2996
QY	2451	CTACAATCGAAGTACGAGGAGCGGTGACAACTCACTTCACTGTACAACTGATCGTCTCA	2510
Db	2997	CTGAACAGGAGATATGAGGCTTTGTCTATGAGCACTTCTTCGGTTAAAAAGTCTGTTTG	3056
QY	2511	TCTGAGATGATAGCGGTAAAGGAGTACTAAACAGTGTTCCTCAACCACTAAAAAGGAAA	2570
Db	3057	CAGGAGATGGTCGCGGAGCGCGTGTATCAATCCGATCTCAAAACCTTCATGATGCAAG	3116
QY	2571	ATTCTAATTTTCACTCAGGCTGATAAATTTGAGTTAGAGGAGAGGCTATAAGATGTG	2630
Db	3117	ATCTGTACTTTTACCCAAATCGGATAAAGAGCTCTGCTTCAAGAGGATATTCAGATGTT	3176
QY	2631	AACACCGTTCAATGAGATCCAAAGGAGAAACCTTTTGAAGATGTGCTGCTCAGATTTGACG	2690
Db	3177	CACACTGTGATGAAGTGAAGGCGAGACATCTCTGATGTTTCACTAGTTAGGTTAAC	3236
QY	2691	GCAACTCACTGACTCTGATTTTCCAACTTCCCGCATGTTCTAGTCGCTCTGACTAGA	2750
Db	3237	CCTACACAGTCTCCATCAITTCAGAGGAGACAGCCCACTGTTTGGTCCGATTTGCAAGG	3296
QY	2751	CACACAAAGAGCTTCAAAATATTACACCGTAGTGTAGATCCTTTAGTACAGATTAATAGT	2810
Db	3297	CACACCTGTTGCTCAAGTACTACACTGTTGTTATGATGCTTTTGTAGTTATCATTAGA	3356
QY	2811	GATTTGTCTTCTTTAAAGCTCTCTTTTAAAGATGATATGTTAGAGCAGAGTAGTAGA	2870
Db	3357	GATCTAGAGAACTTAGTCTGCTGTTTGTAGATGATGATAGGTCGATGAGGAAACACA	3416
QY	2871	TAGCAATTAACAGATGAGTGTCAAAAGTCAATATCTTTTGTGGCAACCTTAA	2930
Db	3417	TAGCAATTAACAGATGAGTGTCAAAAGTGTCAAAAGTGTCAAACTTTTGTGTCAGCGCAAAG	3476
QY	2931	TCAGGAGACTTTCCAGATCTACAGTCTTATACAGTATGCTCCCTGCTGTTAAATAGTACT	2990
Db	3477	ACTGGTATATTTCTGATATGCACTTTTACTATGATAGTGTCTCCAGGCAACAGACAC	3536
QY	2991	ATACCTTAACAGTATGATGCTTTTACCATGAGGTTTACGTGATAATAGTCTTTAAATGTGAAG	3050
Db	3537	ATGATGATTAATTTTGTGCTGTTTACCATGAGGTTGACTGACATTTCACTGAATGTCAA	3596
QY	3051	GATTTGTCTGTTGATTTTCCAAAAAGTATTCGAGATGCCAAAGAGGTTGAAACCATGTCTA	3110
Db	3597	GATTCATATTTGATATGCTTAAGTCTGTTGCTGCGCTAAGGATCAAAATCAAAACCACTA	3656
QY	3111	GAGCCAGTTTTCGTACCGCGCGGNAACCGCCRAAGGCTGCAGGACTACTCGAAAACTCG	3170
Db	3657	ATACCTATGTTACGAAACGGCGGCGAGAAATGCGCCAGACTGCGACTATTTGAAAAATTTA	3716
QY	3171	GTTCCAATGATTTAAAAAGAAATTTCAAGCCACAGACCTGACGGGACGATTTGACATTCAG	3230
Db	3717	GTGGCGATGATTAAGAGAACTTTAAAGCACCAGTTGCTGCACTCATTTGATTTGAA	3776
QY	3231	AGCACCCGATCTGTTGTAGTAGATAAGTTTTGTATGCTATTTTATTTAAAAAGAGAAAA	3290
Db	3777	AATACTGCATCTTTAGTTAGATAAGTTTTGTATGATTTTGTATGTTTGTCTTAAAGAAAAAGA	3836
QY	3291	TACACAAAAATATTTGCTGGAGTGAATCAGAGGATTCATATGATGAGATGTTTGGAAAAAC	3350
Db	3837	AAACCAATAAAAATGTTTCTTTGTTTCACTAGAGAGTCTCTCAATAGATGTTTGAANAAG	3896
QY	3351	AGGAAAGAGTACTTATTTGGACGACTTGGCTAACTTACAAATTTTACAGATCTCCCGGCCATC	3410
Db	3897	CAGGAAACAGGTAAACAAATAGCCACCTCGCAGATTTTGTATTTTGTAGATTTTCCAGCAGTT	3956
QY	3411	GATCAGTACAGCAGATGATCAAGGCTCAAGCCAAAAACAGAAATTTGGACCTTTCAATTCAG	3470
Db	3957	GATCAGTACAGCAGATGATTAAGAGCAACCCCAAGCAAAAAATTTGGACACTTCAATCCAA	4016
QY	3471	AATGAATACCTGCTCTGCAAAACAATTTGTTCTACCATTCGAAGCAGATCAACGGTATTTTG	3530

Db 4017 ACAGGATACCGGCTTTCAGACGATTTGTACCAATCAAAAAGATCAATGCAATATT 4076
Qy 3531 GCCGGTTCT--CAGAGCTTACAGGTTGCTCGAGGCAATTTGATTCTTAAGAGTTT 3587
Db 4077 GCGCCGTTGTTAGTGAGCTTACTAGGCAATTTACTGGACAGTGTGTTGATTCGAGCGATTT 4136
Qy 3588 CTTTCTTTTACTAGGAAACTCCAGAACAGATTCAGAAATTTTCTCGGATCTCGACTCG 3647
Db 4137 TTGTTTTTCAAGAAAGACACCGCGAGATTTAGGATTTCTTCGGAGATCTCGACAGT 4196
Qy 3648 CAGCTTCTTCTAGGATGTGTAAGACTGGATATTTCTTAAGTATGATTAAGTCAAGAACGAG 3707
Db 4197 CATGTGCCGATGATGTCTGAGCTGATATCAAAATACGACAAATCTCAGAATGAA 4256
Qy 3708 TTTCTATGCTGTAGATGATGAATATGAAAGATTTGGGTCTCAATGAGTTTTTGGCC 3767
Db 4257 TTCCACTGTGAGTAGAATACAGATCTGGCGAAGATTTGGGTTTGAAGACTTCTTGGGA 4316
Qy 3768 GAAGTGTGAAACAGGGCACAGGAAACCAACTTTGAAGGATTACATTTCTGGAATCAAG 3827
Db 4317 GAAGTTTGAAGAACAGGGCATAGAAGACCCCTCAAGGATTTACCGCAGGTATATAA 4376
Qy 3828 ACATGCTGTGTATCAAGGAAAGCGGTGATGATCTTTCTCATCGGCAATATCTGTT 3887
Db 4377 ACTTGCATCTGTATCAAGAAAGAGCGGGACGTCACGACGTTCTANTGGAAACACTGTG 4436
Qy 3888 ATATAGAGCTGCTTGGGTTCAATGTTACGATGGAAGAGTTCATAAAGGTCCTTT 3947
Db 4437 ATCATTTGCTGATGTTTGGCCCTCGATCTCGATTTGGGAAATATCAAGGAGCCCTT 4496
Qy 3948 TGTGAGAGCATTCGGTTTGTATTTCCAAAGGTTTGGATTTCCCTGACATTCAGTCA 4007
Db 4497 TCGGTGAGATGATGCTGCTGCTTCTTCCAAAGGTTTGGAGTTTCCGGATGTGCAAC 4556
Qy 4008 TGTGCTAATCTCATGTGGAATTTTGAAGGCAAACTGTATAGAAAGGATACGTTACTTT 4067
Db 4557 TCCGCAATCTTATGTGGAATTTTGAAGCAAACTGTTTAAAGAACAGTATGATCTTT 4616
Qy 4068 TGTGTAGATACATCATACATGATAGGAGCAATAGTGTATATGATCTTTGAG 4127
Db 4617 TCGGGAAGATATGTAATACATCAGCAGAGGATGCAATTTGTATTAACGATCCCTTAAAG 4676
Qy 4128 TTGATCTCAAACTTGGGCAAAACATATCAGGATTTATGATCATTAGAAGGTTAAGG 4187
Db 4677 TTGATCTCGAACTTGGTGCTTAAACATCAGAGATTTGGAAACATTTGGAGGATTCAG 4736
Qy 4188 GTGTCTTTGTGCGATGTTGCTTGTCTCGCTCGGAACTGTTGCTTAGGCTTTCCGCGAGT 4247
Db 4737 AGGTCTTTTGTGATGTTGCTGTTTCTGTT--GAACAATTTGCGTATTACACAGTTG 4793
Qy 4248 AACGAGCTATCAAGAGGTTTCAAAACCGGATTTGATGTTGTTGCTTTTAAATGTT 4307
Db 4794 GACGACGCTGTATGGAGGTTTCAAGAGCGCCCTCCAGGTTGTTGTTTATAAAGT 4853
Qy 4308 GTTACAAATTTTGTGCTGATAATTTTATTTATAGAACTTTGTTTAAATGCTGTTAG 4367
Db 4854 CTGGTGAAGTATTTGCTGATAAAGTTCTTTTAGAAGTTTGTATAGATGCTCTAGT 4913
Qy 4368 TCTCAGAGATCTGTCAAAATTTAGCGAGTTTCATTTGATCTTTTGAAGAGGATGAGATCT 4427
Db 4914 TGTAAAGGAAAGTGAATATCAATGATTTATCGCTTACGCTGACAAAATGAGAGATCTT 4973
Qy 4428 TCGGCAATTCAGCTAAGGTCAAGAGTGTAGAAATATCGACTGTGCAAGATTTATGCG 4487
Db 4974 ACCGTGATGTTTACCCCTGTAAGAGTGTATGTTGTTCCAAAGTTTGAATAAATGTT 5033
Qy 4488 TGTAAAGATGATGCTTCTGATGATTTTACTTAAAGGTTTAAAGTTAGTTAGTAA 4547
Db 5034 TCATGAAGATGATGCTTATGTCAGAGGTGAACCTTCTTAAAGGAGTTAAGCTTTATGAT 5093
Qy 4548 AGGATGATGCTTAGCTGATTTGTTAGTGTCTGGGAGTGAATCTCCCGGATTAACGT 4607

Db 5094 TGGATACGTCTGTTTACCGGTTTGGTCTGTCACGGCGAGTGGAACCTTGCCTGACAAATTG 5153
Qy 4608 CCGTGGTGGTCTCAGTGTGTTGTTATTTAGATTAAGAAATGAAAGAGTAAAGGAAAC 4667
Db 5154 CAGAGGAGTCTGAGCGTGTCTCTGGTGGAACAAAGAGTGAAGAGCCGACGAGCCAC 5213
Qy 4668 GCTGGTGGTATCAGCGCCCTGCTTGCACAAAGAAATTTTCTTTTAAGCTAAATCCCTAA 4727
Db 5214 TCTGGATCTTTACTACACAGCAGCTGCAAGAAAGATTTGAGTTCAAGGCTGTTCCCA 5273
Qy 4728 TTATTTCAATACATCCGAGGATGCTGAGAACCCCGTGGCAAGTGTAGTGAATATCAA 4787
Db 5274 TTATGCTATAACACCCAGGACGCGATGAAACCGTCTGGCAAGTTTGTAGTTAATATTAG 5333
Qy 4788 AGGAGTGGCTATGGAAGAGGATACGTGCTTTTATCTTTTGGAGTTCGTTTCAATTTGTT 4847
Db 5334 AAATGTGAAGATGTCAGCGGTTTCTGTCGCTTCTCTCGAGTTTGTGTCGGTGTAT 5393
Qy 4848 AGTACATAAATAATGTAAGAAAGTTTGAAGGACGTATTTTGGAGTGAAGTACCAATGCG 4907
Db 5394 TGTATTAGAATAATATAAATAATAGGTTTGAAGAGAGATTAACAACGTGAGAGCGG 5453
Qy 4908 CTCGCCAATTCGAACCTCACTGAAAGGTTTGGAGGATTCGTTGGATGAAGTACCAATGCG 4967
Db 5454 AGGGCCCATGGAATTCACAGAGAGTGTGATGATGATGATGATGATGATGATGATGAT 5513
Qy 4968 TGTGA 4972
Db 5514 GATCA 5518

RESULT 10

US-09-401-415-2
; Sequence 2, Application US/09401415
; Patent No. 6503732
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS TO
; OVERPRODUCE PEPTIDES AND PROTEINS

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: Spensley Horn Juntas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/401,415
FILING DATE: 21-Sep-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01467
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Bostich, June M.
REGISTRATION NUMBER: 31,238
REFERENCE/DOCKET NUMBER: PD-4074

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 6395 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

2517	CGAAA	CGGAGAA	CCGCATGTCAGTAGCGCAAGGTTGTTCTTGTGACGAGATTCGGGC	2576
2040	TGTGGAAAGTA	CAAAGGAGATTTT	TGAAAGATTTTGATCTTGATGAGGATTTTGATCTTTGGTT	2099
2577	TGTGGGAAAA	CCAAAGAAA	TTCTTTTCAGGGTTAAATTTTGCATGAAGATCTAAATTTTAGTA	2636
2100	CCTGGAAAA	CAAGCTGCTGCTATGATCAGAAGAGGGCTAA	TTCACTGCGACTGATAAGA	2159
2637	CCTGGGAAGCA	AGCCGCGAAATGATCAGAAGACGTGCGAA	TTCTCAGGGATTAATTGTG	2696
2160	GCCCAATGCA	CAATGTGAGAA	CGGTAGATTTCACTTCTAATGCAAT-----CCAAAA	2210
2697	GCCACGAGGAC	CAACGTTAAA	CCGTGATTTCTTTCAATGATGAATTTTGGAAAAACACA	2756
2211	CCGCGATCACA	CAAGAGGCTTTTT	TAATGATGAAGGTTGATGTGCAACACCGGTTGTGTT	2270
2757	CGCTGT	CAGTTCAAGAGGTTATTCATTTGATGAAGGGTTGATGTTGCAT	ACTGCTGTGTTT	2816
2271	AAC	TTCTCTGTGCTTTATCTCTGTTTGGCAATCGCATACATATTTACGGAGATACACAGCAG		2330
2817	AAATTTCT	TGTGGCGATGTCAITTTGTGCGAAATTTGCATATGTTTACGGAGACACACAGCAG		2876
2331	ATTCTTTT	CATTAAACAGAGTTCCAGAA	TTTTCCCGTATCCCAAACATTTTGTGAGAAGCTGCAA	2390
2877	ATTCATACAT	CAATAGAGTTTCAGAA	TTCCCGTACCCCGCCCAATTTTGGCAATTTGGAA	2936
2391	GTGATGAA	GTGATGAGGAGGACACACACTGAGATGCCAGGTGATGTGAATTTTTTC		2450
2937	GTTGACAGG	TGGAGACACGCAAACTACTCTCCGTTGTCCAGCCGATGTACACATTAT		2996
2451	CTACAATCGA	AGTAACGAAGAGCGGTGACAAACCACTTCAACTGTACAACGATCGGTCTCA		2510
2997	CTGAA	CAGGAGATATGAGGGCTTTGTCA	TGAGCACCTTCTTCGGTTAAAAAGTCTGTTTCG	3056
2511	TCTGAGATGAT	AGCGGTAAAGGAGTACTAAACAGTGTTC	CCAAAACCACTAAAGGGAAA	2570
3057	CAGGAGATG	TGCGCGAGCGCGGTGATCAATCCGATCTCA	AAACCCCTTGCATGGCAAG	3116
2571	ATTGTAAC	TTTTCACTCAGGCTGATAAAATTTGAGTTAGAGGAGAGGGCTATAAGAATGTG		2630
3117	ATCTGACT	TTTTACCCAAATCGGATAAGAGACTCTGCTTTCAAGAGGGTAATCAGATGTT		3176
2631	AACACCG	TTCAATGAGATCCAAAGGAGAAA	CCTTTGAAGATGTGTCGTGTGTCAGATTGACG	2690
3177	CACACTGTG	ATGAAGTGAAGGCGAGACATACTCTGATGTTTCACTAGTTAGGTTAAACC		3236
2691	GCAACTCCA	CTGACTGTGATTTCCAAGTCTTCCCGCATGTTT	TAGTCGCTCTGACTAGA	2750
3237	CCTACAC	CCAGTCTCCATTTTGCAGGAGACAGCCCA	CATGTTTGTGTCGCAATTTGTCAAGG	3296
2751	CACACAA	AGAGCTTCAAAATATTACACCGTAGTGT	TTAGATCCCTTTAGTACAGATAATTAGT	2810
3297	CACAC	CTGTTCCGCTCAAGTACTACATGTTTGTAT	TGGATCTTTTAGTAGTATCATTTAGA	3356
2811	GATTTGT	CTTTTAAAGCTCCTTCTTTTAAAGATGTATATG	TGTAGAGCAGGTAGTAGA	2870
3357	GATCTAG	AAAACTTAGCTCGTACTTCTGTTAGATATGT	ATAAGGTGATGAGGAAACACAA	3416
2871	TAGCAAT	TACAGATGATGCGATGTTCAAAAGGTCA	TAATCTCTTTTGGGCAACACCTAAA	2930
3417	TAGCAAT	TACAGATGATGCTCGGTGTTTCAAAAGG	TTTCCAATCTTTTGTGAGCGGCCAAAG	3476
2931	TCAGGAG	CTTTCCAGATCTACAGTCTTATTTACAGATGT	ATGCTCCCTCGTGAATAGTACT	2990
3477	ACTGGT	GATATTTCTGATATGCAGTGTTTCTATGAT	TAAGTGTCTCCAGGCAACAGCACCC	3536
2991	ATAC	TTAAACAGTAGTATGCTGTTTACCATGAGG	TTACGTGATATAGTCTTAATGTGAAG	3050
3537	ATGATGA	ATAATTTTGTATGCTGTATCCATGAGG	TTTGACTGACATTTCAATGAATGCAAA	3596
3051	GATTTGT	GTCTTTTCAAAAGTATTTCCGATGCAAG	GGTGAACCAATGTCTA	3110
3597	GATTTG	CATATTTGGAATATGTCTAAGTCTGTTG	CTGCTCGCTAAGGATCAAAATCAAAACACTA	3656

QY	3111	GAGCCAGT	TTTTCGTACCGCGCGGGAACCGCCAAAGGCTCGAGACTACTCGAANAATCTG	31170
DB	3657	ATACCTATGGTACGAACCGCGCGCAGAAATGCCACGCCAGACTGGACTATTTGGAAAAATTTA	3716	
QY	3171	GTTTCAATGATTAAGAAGAAATTTCAACGCGACCCAGACCTGACGGGGACGATTGACATTTGAG	3230	
DB	3717	GTGGGGATGATTAAGAAGAACTTTAAACGCCACCCGAGTTGTCTGSCATCATTTGATATTGAA	3776	
QY	3231	AGCACCGGACTGTTGTAGTAGATAAGTTTTTTTGTATAGCTATTTTATTAAAAAAGAAAAA	3290	
DB	3777	AATACTCGATCTTTAGTTGTAGATAAGTTTTTTTGTATAGTTATTTTGTCTTAAAGAAAAAAGA	3836	
QY	3291	TACAAAAAATAATGTCTGGAGTGATGCAAGAGGATTCAAATGATGAGATGGTTGGAAAAAC	3350	
DB	3837	AAACCAATAAANAATGTTTCTTTGTTTCAGTAGAGAGTCTCTCAATAGATGGTTAGAAAAAG	3896	
QY	3351	AGSAAAGAGPACTATTTGGACGACTTGGCTTAACCTACAATTTTACAGATCTGCCGGCCATC	3410	
DB	3897	CAGGAAACAGGTAAACAAATAGGCCAGCTCGCAGATTTTGTATTTGTGTAGATTTTGCACGACGTT	3956	
QY	3411	GATCAGTACAGACATGATCMAAGCTCAACCAAAACAGAAAAATGGACCTTCCAATTCAG	3470	
DB	3957	GATCAGTACAGACATGATTAAGCAACACCCCAAGCAAAAATTTGGACCTTCAATCCAA	4016	
QY	3471	AATGAATAACCTGCTCTGC AAAACAATTTGTCTTACCATTTGAAAGCAGATCAACGGTATTTTG	3530	
DB	4017	ACGGAGTACCGGCTTTTGCAGACGATTTGTACCATTTCAAAAAGATCAATGCAATATTT	4076	
QY	3531	CCCGGTTTCT---CAGAGCTTACAAGTTTGTGCTCGAGGCATTTGATTTCTAAGAAGTTT	3587	
DB	4077	GGCCGTTGTTTGTAGTGAGCTTACTAGGCAATTAATGGACAGTGTGTAATCGACACAGATTT	4136	
QY	3588	CTTTTCTTTACTAGAAAACTCCAGAAACAGATTCAGAAATTTTTTCTCGGATCTCGACTCG	3647	
DB	4137	TTGTTTTTCAAGAAAGACACCGCCAGATTCAGGATTTCTTCGAGATCTCGACAGT	4196	
QY	3648	CACGTTCTATPGATGTGTAGAACTCGATATTTTCTAAGTATGATAAGTCAAGAACGAG	3707	
DB	4197	CATGTGCGATGGATGTCTTGGAGCTGGATATATCAAAATACGACAAATCTCAGAAATGAA	4256	
QY	3708	TTTTCAATTTGCTGTAGAGTAGTAANAATGAAAGATTTGGTCTCAATGAGTTTTTGGCC	3767	
DB	4257	TTCCACTGTGCGATGAGTAATACGAGATCTGGGAAGATTTGGTTTTTGAAGACTTCTTGGGA	4316	
QY	3768	GAACTGTGGAACAAGGCGCACAGAAAAACAATTTGAAGGATTACATTTGCTGGAATCAAG	3827	
DB	4317	GAGTTTGGAAAAACAAGGCGCATAGAAAGACCACTCAAGGATTAATCCGACAGGTATAAAA	4376	
QY	3828	ACATGCTGTGGTATCAAGGAAAGCGGTGATGTGACTACTTTTCATCGGCAATACTGTT	3887	
DB	4377	ACTTGGCATCTGGTATCAAGAAAGAGCGGGACGTCACGCGTTTCATTTGGAACAACACTGTG	4436	
QY	3888	ATAATAGCAGCTTCTTTGGGTTCAATGTTACCGATGAAAAAGGTCATAAAAGGTGCTTTTT	3947	
DB	4437	ATCAITGCTGCAATGTTTGGCTCGATGCTTCCGATGAGAAAAATATCAAGAGNGCCTTT	4496	
QY	3948	TGTGGAGACGATCCGTTTTGTATTTTCCAAAGGTTTTGGATTTCCCTGACATTCAGTCA	4007	
DB	4497	TGCGGTGACGATAGTCTGCTGACTTTTCCAAAGGTTTGTGAGTTTCCGGATGTGCAACAC	4556	
QY	4008	TGTGCTAATCTCATGTGGAATTTTGGGCCAAACTGTATAGAAGAGGTACGGTTACTTTT	4067	
DB	4557	TCCCGGAATCTTATGTGGAATTTTGAAGCAAAACTGTTTAAAAACAAGTATGNAATCTTT	4616	
QY	4068	TGTGTAGATACATCATACCATGATAAGGGAGCAATAGTGTATTTATGATCTCTTGAAG	4127	
DB	4617	TGCGGAAGATATGTAATACATCACGACAGAGGATGCATTTGTATTAACGATCCCTAAAG	4676	
QY	4128	TTGATCTCCAAACTTTGGGCGAAAACATATCAAGATTTATGATCACTTTAGAGAGTTAAGG	4187	
DB	4677	TTGATCTCGAACTTTGGTGTGTAACACATCAAGGATTTGGGAACAATCTTGGAGGAGTTCCAGA	4736	

Db 3237 CCUACACGAGUCUCCAUUUGUAGGAGAGACAGCCCAUGUUUUUGGUGCAUUGUCAAGG 3296
Qy 2751 CACACAAAGAGCTTCAAATATTTACACCGTAGTGTGTAGATCCTTTTGTAGTACAGATAATTAGT 2810
Db 3297 CACACCUUGUGCUCAAGUACUACACUGUUGUUAUGGAGUCCUUGUUAUGUUAUUA 3356
Qy 2811 GATTGTCTCTTTAAAGCTCTCTTCTTTTGAAGATGTATGTGTAGAGCAGGTAGTAGA 2870
Db 3357 GAUCUAGAGAAA CUUAGUCGUUACUUGUUAUGUUAUGUUAAGUGUGUGAGCAGGACAA 3416
Qy 2871 TAGCAATTAACAGATGAGTGTCTCAAGGTCTATAATCTCTTTGTGGCAACACCTAAA 2930
Db 3417 UAGCAUUAACAGAUUGAGUCUGUGUGUUAAGUGUCCAAUCCUUUUUGUGGAGCCCAAG 3476
Qy 2931 TCAGGAGACTTTCCAGATCTACAGTCTTATTTACGATGTATGCTCCCTCGTGTAACT 2990
Db 3477 ACUGUGAUUUUCUGAUUUGCAGUUUAUUAUUAUUAAGUGUCUCCCGAGCAACAGCAC 3536
Qy 2991 ATACTTAAAGATGATGCTGTACCATGAGGTTCGTGATTAATAGTCTTAAATGTGAAG 3050
Db 3537 AUGAUGAAUUAUUUGAUGUGUUAUCCAUAGGUGUGACUGACA UUUUUAUUGAAUUGCAA 3596
Qy 3051 GATTGTCTCTTGTATTTTCCAAAGTATTTCCGATGCCAAGGAGGTGAACCATGTCTA 3110
Db 3597 GAUUGCAUUAUGGAUUGUCUAUGUCUGUGUGCGCCUUAAGGAUUAUUAUUAUUAUUA 3656
Qy 3111 GAGCCAGTTTTCGCTACCGCGCGGAAACCGCAAGGCTGACGACTACTCGAAAACTGT 3170
Db 3657 AUACCUAUGUACGAAACCGCGCGCAGAAUGCCAGCAGACUGGACUAUUGGAUUAUUA 3716
Qy 3171 GTTCGAATGATTAAGAAATTTCAACGCACAGACCTGACGGGAGCATTTGACATTTGAG 3230
Db 3717 GUGCGAUGAUUUAAGAGAA CUUUAACGCACCCGAGUUGUGUGCAUUGAUUUAUUGAA 3776
Qy 3231 AGCACCCATCTGTTGTAGTAGATAAGTTTTCATAGCTATTTTATTAAGAAAGAAAAA 3290
Db 3777 AAUACUGAUCUUUAGUUGUUAAGAUUUUUUGAUUUAUUGUUAUUAUUAUUAUUAUUA 3836
Qy 3291 TACACAAAAATATTTGCTGGAGTATGACGAAGGATTCATATGATGAGATGTTTGGAAAC 3350
Db 3837 AAACCAUAAAAUUGUUCUUGUACUAGAGAGAGUCUCUCAAUAGAUUGUUAUUAUUA 3896
Qy 3351 AGGAAGAGTACTATTGGAGCAGCTTGCTGCTAACTTACATTTTACAGATCTCCCGGCATC 3410
Db 3897 CAGGAACAGGUACAAUAGGCGCAGCUCGACAUUUUGAUUUUGUUAUUGCCAGCAGUU 3956
Qy 3411 GATCAGTACAAGCAGATCATCAAGCTCAACCAAAACAGAAATTTGGACTTTTCAATTTCAG 3470
Db 3957 GAUCAGUACAGACAUUAUUAAGCAACACCCAGCAAAAUAUUGGACAUUUAUUAUUA 4016
Qy 3471 AATGAATACCCCTGCTGCAAAACAAATTTGTACCATTCGAAGCAGATCAACGGTATTTTG 3530
Db 4017 ACGGAGUACCCGGCUUGUACAGCAGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4076
Qy 3531 GCCGGTTCT---CAGAGCTTACAGGTTGCTGCTGAGGCAATTTGATCTTAAGAGTTT 3587
Db 4077 GCGCGUUGUUAUGUAGCUUACUAGGCAUUAUUGGACAGUUGUUAUUAUUAUUAUUAU 4136
Qy 3588 CTTTCTTTTACTAGGAACCTCCAGAACAGATTCAGAAATTTTCTCGATCTCGACTCG 3647
Db 4137 UGUUUUUUACAAAGAAACACACCGCGAGAUUGGAAUUAUUAUUAUUAUUAUUAUUAU 4196
Qy 3648 CACGTTCTCTTGGATGTTTGAAGCTGATATTTCTAAAGTATGATTAAGTCAACAGAACGAG 3707
Db 4197 CAUGUGCGAUGGAGUUGUUGGAGCUGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4256
Qy 3708 TTTCTATTGCTGTAGATGATGAATATGGAAGATTTGGGTCTCAATGAGTTTGTGCC 3767
Db 4257 UUUCAUGUGAGUAGAAUAUCAGAUUCUGGCAAGAUUGGUGUUAUUAUUAUUAUUAU 4316
Qy 3768 GAAGTGTGAAACAGGCGCACAGGAAAAACATTTTGAAGGATTTACATTTGCTGGAAATCAAG 3827
Db 4317 GAAGUUUGAAACAAAGGCAUUNGAAGAACCCCUACAGGAUUAUUAUUAUUAUUAUUA 4376

Qy 3828 ACATGCTGTGTGTATCAAAGGAAAAAGGGTGATGTGACTACTTTTTCATCGCAATACTGTT 3887
Db 4377 ACUUGCAUCUGGUUAUCAAAGAAAGACGGGGAGCGUACGACGUUAUUAUUAUUAUUA 4436
Qy 3888 ATAATAGCAGCTTGTGGTGTCAATGTTTACCGATGGAAAGGTTCATAAAAGGTGCTTTT 3947
Db 4437 AUCAUUGUGCAUUGUUGGCUUGCUUCCAAAGGGUUGAGUUUCGGAUGUGCAACAC 4496
Qy 3948 TGTGGAGACGATTCCTGTTTGTATTTTCCAAAGGGTTTGGATTTTCCCTGACATTCAGTCA 4007
Db 4497 UGCGUGACGAUAGUCUGUGUACUUUCCAAAGGGUUGAGUUUCGGAUGUGCAACAC 4556
Qy 4008 TGTGCTTAATCTCATGTGGAAATTTTGGGCCCAAACTGTATAGAAGAGGTACGGTTACTT 4067
Db 4557 UCGCGGAUUCUUGUGGAAUUAUUGAACAAACUGUUUAAAAACAGAUUGGAUUAUU 4616
Qy 4068 TGTGGTAGATACATACATACACCATGATAAGGGAGCAATAGTGTATTAATGATTCCTTTGAAG 4127
Db 4617 UGCGGAAGAUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4676
Qy 4128 TTGATCTTCCAAACTTGGGGCAAAACATATCAAGGATTTATCATCTTTAGAGAGTTAAGG 4187
Db 4677 UUGAUUCUGGAAACUUGGUGCUAAACACAUCAGGAUUGGGAACACUUGGAGGAGUUCAGA 4736
Qy 4188 GTGTCTTTGTGCGATGTTGTTGTCGTCGGAACCTGTGTGCTTGTAGGCTTTCCGACGTG 4247
Db 4737 AGGUCUCUUGUGAUGUGUGUUCUUUU---GAACAAUUGUGCGUUAUUAUUAUUAUUA 4793
Qy 4248 AACGCAGCTATCAAGGAGTTTCAAAAAACCGCGATTCATGTTGTTGCTTTTAAATGT 4307
Db 4794 GACGACGCUUUGGAGGUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4853
Qy 4308 GTTAAACAAATTTTGTGTGATAAATTTTATTTAGAACTTTGTTTAAATTTGCTGTTAG 4367
Db 4854 CUGGUGAAGUUAUUGUCUGAUAAAGUUUUUUAAGAUUUUUUAUUAUUAUUAUUAUUA 4913
Qy 4368 TCTCAGAGATCTGTCAAATTTAGCAGTTTCATTGATCTTTTCGAAACAGGATGAGTACT 4427
Db 4914 UGUUAAAGGAAAGUGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4973
Qy 4428 TCCGGCATTCATGACTAAGGTCAAGAGTGTAGAAATATCGACTGTGGACAGATTTATGGC 4487
Db 4974 ACCGUCAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5033
Qy 4488 TGTTAAGAATGATAGTCTTTCTGATGATGATTTTACTTAAAGGTGTTAGTTAGTTAAGAA 4547
Db 5034 UCAUGAGAAUGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5093
Qy 4548 AGGTATGTGTGCTTGTAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 4607
Db 5094 UGGAUACGUCUGUUUACCGGUGUGUGUACCGGCGAGUGGAAUUAUUAUUAUUAUUAUUA 5153
Qy 4608 CCGTGTGTGTGCTGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 4667
Db 5154 CAGAGAGGUGUGAGCGUG 5213
Qy 4668 GCTGGTGCCTGATCACGCCCTGCTTGCAAAAGAAATTTTCTTTTAAAGCTTAATCCCTAA 4727
Db 5214 UCUCGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5273
Qy 4728 TTATTCAATAACATCCGAGGATGCTGAGACACCCCTGGCAAGTGTGTAGTGAATATCAA 4787
Db 5274 UUAUGCUAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5333
Qy 4788 AGGAGTGTGCTATGGAAGAGGATGCTGCTCTTTTATCTTTTGGAGTTTCTTTCAATTTGT 4847
Db 5334 AAUUGAAGAGUAGUCAGCGGUGUUCUGUCCUUAUUAUUAUUAUUAUUAUUAUUAUUA 5393
Qy 4848 AGTACATAAAATTAATGTAAAGAAAGTTTGGGGAAAGTATTTTGTAGTGTGACAGACGG 4907
Db 5394 UGUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5453

3957 GAUCAGUACAGACACAGUAAUAAAGCACACACCAACCAAAAAUUGGACACUUAUCCAA 4016
QY
3471 AATGAATACCCCTGCTCTGCAAAATTTGCTACCATTCCTGAAGCAGATCAACGATTTTG 3530
Db
4017 ACGGAGUACCCGCGUUGGAGAGAGUUGUUGUACCAUCAAAGAAAGUAAUUAUU 4076
QY
3531 GCCGGTTCT--CAGAGCTTACAAGGTTGCTGCGAGGCAATTTGATTTAAGAGTTT 3587
Db
4077 GCGCCGUGUUGUAGUGAGCUUACUAGGCAAUUACUGGACAGUUGUUGUUGAGCAGAUU 4136
QY
3588 CTTTCTTTTCTAGGAAACTCGAGAAACAGATTCAGAAATTTTCTCGATCTCGACTCG 3647
Db
4137 UUGUUUUUACAGAAAGACACCGAGCGAGUUGAGGAUUUUUUUUGGAGUUCUGCAGU 4196
QY
3648 CAGGTTCTGATGATGTTAGAACTGAGATTTCTTAAGTATGATGATGATGATGATGAT 3707
Db
4197 CAUGGCGGAGUAGUUGUUGGAGCGUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUA 4256
QY
3708 TTTCAATTTGCTGTAGAGTATGAATATGGAAGATTTGGGCTCTCAATGAGTTTGGCC 3767
Db
4257 UUCCACUGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 4316
QY
3768 GAAGTGTGAAACAAGGCGACAGGAAACAACTTTGAAGATTAATTTCTGCTGAATCAAG 3827
Db
4317 GAAGUUGGAAACAAGGCGAUAAAGACACCCUUAAGGAUUAUUAUUAUUAUUAUUAUUA 4376
QY
3828 ACATGCTGCTGTATCAGAGGAAAGCGGTGATGATGATGATGATGATGATGATGATGAT 3887
Db
4377 ACUGGAGUUGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 4436
QY
3888 ATAATAGCAGCTGCTGTTGGTTCATATGTTACCGATGGAAGAGTCTATAAAGGTTGCTTT 3947
Db
4437 AUCAUUGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 4496
QY
3948 TGTGAGAGAGTTCCTGTTGTTATTTTCCAAGGTTTGGATTTCCCTGACATTCAGTCA 4007
Db
4497 UGCGGAGCAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 4556
QY
4008 TGTGCTAATCTATGTTGGAATTTTGAAGGCAACTGTATGAGAGAGGTTACGTTACTTT 4067
Db
4557 UCGCGAAUUAUUGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 4616
QY
4068 TGTGTPAGATACATACATACATGATGAGGAGCAATGATGATGATGATGATGATGATGAT 4127
Db
4617 UGCGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 4676
QY
4128 TTGATCTCCAACTTCGGGCAAAACATATCAAGATTTATGATCATTAGAGAGTTAAGG 4187
Db
4677 UUGAUCUCGAAACUUGGUGCUAAACACUACAGGAGUUGGAAACACUUGGAGGAGUUC 4736
QY
4188 GTGCTTTTGTGCGATGTTGTTGCTCGGAACTGTTGCTGTTAGGCTTCCGAGCTG 4247
Db
4737 AGGUCUCUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 4793
QY
4248 AACGAGCTATCAAGAGGTTTCAAAAACCGGATTTGATGTTGCTGTTGTTTAAATTTG 4307
Db
4794 GAGGAGCUGUAGGAGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 4853
QY
4308 GTTAAACAAATTTTGTGTGATAATTTTATTTAGAACCTTTGTTTAAATGCTGTTAG 4367
Db
4854 CUGGUGAAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 4913
QY
4368 TCTCAGAGATCTGTCAAAATTTAGCGATTCATTTCTTCAAAACAGGATGAGATCT 4427
Db
4914 UGUUAAAGGAAAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 4973
QY
4428 TCCGGATTCATGACTAAGTCAAGTGTAGATATGATGATGATGATGATGATGATGATGAT 4487
Db
4974 ACCGUGAUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 5033
QY
4488 TGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4547
Db
5034 UCAUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 5093

QY 4548 AGGATATGTTGCTTTAGCTGATTTTGGTATGTTCTGGGAGTGAATCTCCCGATACTG 4607
Db
5094 UGGAUACGUCUGUUAUAGCCGUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUG 5153
QY 4608 CGGTGTTGTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 4667
Db
5154 CAGAGGAGGU 5213
QY 4668 GCTGGTGGTATCACGCCCTGCTTGCAAAAAGAAATTTTCTTTAAGCTAATCCCTAA 4727
Db
5214 UCUCGAGUUCUACUACAGCAGCUGCAAGAAAGAAAGUUAUUAUUAUUAUUAUUAU 5273
QY 4728 TTATTCAATAACATCCGAGATGCTGAGAAAGCACCCTGCGCAAGTGTGTTAGTGAATCAA 4787
Db
5274 UUAUGCUAUAACCAACCCAGGACCGCAUAGAAAAACGUCUGGCAAGUUAUUAUUAU 5333
QY 4788 AGGAGTGGCTATGGAAGAGGATCTGCTTTATCTTTTGGAGTTCGTTTCAATTTGCT 4847
Db
5334 AAAUGGAGAGU 5393
QY 4848 AGTACATAAAATAATGTAAGAAAGGTTTGAAGGAAACGTAATTTTGAAGTGTGACACG 4907
Db
5394 UGUUUAUAGAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5453
QY 4908 CTGCGCAATTTGAACCTCACTGAAAGAGTGTGTTGAGGAGTTCGTTGAGTGAAGTACCAATGC 4967
Db
5454 AGGCGCCCAUGGAACUACAGAGAAAGUCGUGAUGAGUUAUGAUGAGUCCUUAUG 5513
QY 4968 TGTGA 4972
Db 5514 GAUCA 5518

RESULT 13

US-09-466-422-3
; Sequence 3, Application US/09466422
; Patent No. 6303779

GENERAL INFORMATION:

APPLICANT: GARGER, STEPHEN
HOLTZ, R. BARRY
MCULLOCH, MICHAEL
TURPEN, THOMAS

TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
FROM PLANT SOURCES

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/466,422

FILING DATE: 17-Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/037,751

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P

REGISTRATION NUMBER: 25,277

REFERENCE/DOCKET NUMBER: 00801.0140.999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-463-8109

TELEFAX: 650-463-8400

; TELEX: <Unknown>		
; INFORMATION FOR SEQ ID NO: 3:		
; SEQUENCE CHARACTERISTICS:		
; LENGTH: 6425 base pairs		
; TYPE: nucleic acid		
; STRANDEDNESS: single		
; TOPOLOGY: unknown		
; MOLECULE TYPE: Genomic RNA		
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:		
US-09-466-422-3		
Query Match	40.8%;	Score 2031; DB 3; Length 6425;
Best Local Similarity	44.4%;	Pred. No. 0;
Matches 2212; Conservative 957; Mismatches 1795; Indels 21; Gaps 4;		
Qy	6	AAGTAAATTCCTGAGTTTCAAAGGAGGCTTTTAAACAGGTATGACAGGTCTCCCAACGAA 65
Db	537	AAAACAGUCCCAACUCCRAAAGGAAGCAUUUGACAGAUACGCAGAAUUCUGAAGAC 596
Qy	66	GTCTGCTGCTCTAAACCTTTTTCAGGATGTGCAATATCATCCGCCAGAGATAGTGGTAGA 125
Db	597	GCUGUCUGUACAUAUUCGACAAUGCGACAUGCGAGCAUGCGCAUGCGCAUCAAGGCAGA 656
Qy	126	AGATACGCTGTGCTCGACAGTTTGTATGATATCTCTGTGCATGAGTTTGGAGCTGCG 185
Db	657	GUGUAGCCUUUGCGCUACACAGCAUAUUGACAUACCGCCGAUGAGUUUGGGGGCGCA 716
Qy	186	TTAATATCTAAGATATACATGTATGTATGTCAGCTTCCATTTTGGCAGAGCAATTATTA 245
Db	717	CUCUUGAGGAAAUAUGUACUACGUGCUAUGCCUUUCUUCUUCUGAGAACCCUGCUU 776
Qy	246	CTAGACGACGAGGTACGCTTAATGAATAGGCGCAACTTTCAAAGAGAGAGGTGAT 305
Db	777	CUUGAAGAUCAUACGUCAAUUGGACGAAAUCAACCGUGUUUUCGCGCGAUGGAGAC 836
Qy	306	GATGTTCTTTTCTTGTGCTGAAGTACTTTAAATATATAGTCAATAACAAAT 365
Db	837	AAGUUGACCUUUUUCUUUGCAUCAGAGAGUACUCUAAUUAUUGCUAUAUUCUUAU 896
Qy	366	ATCTTGCAATATAGTAAATCTTACTTCTCTCTCTAGTAGAATAGTTTACTTTAAG 425
Db	897	AUUCUUAAGUAGUGUGCAAAACUUAUUCUCCGCCUCUAUAGAGAGGUUAUACUAG 956
Qy	426	GAATTTTGTAGTCACTAGGTTTAACTTGTGTTTGTAAATTTA CAAAGTAGATACCTAT 485
Db	957	GAGUUUUUAGUCACAGAGUUUAUACCGUGUUUUGAAGUUUUCUAGAAUAGAUUUUU 1016
Qy	486	ATTCTGTACAGAGTGTAGCAAGTAGGTTGTATAGTGTATGATCTATAGCGCGATG 545
Db	1017	CUUUUGUACAAAGGUGUGGCCCUAAAGUAGUAGUAGUGAGGAGCUUUUUUACUGCAUG 1076
Qy	546	GAAGACGCTTTGCTTACAAGAAACCTTTGGCCATGTTTCAACACTGAAAGAGCAATCTTT 605
Db	1077	GAAGCGCAUGGCAUUAACAAAGACUUCUUGCAUGUGCAACAGCGAGAGAAUCCUCCUU 1136
Qy	606	AGAGACAGGCTTCGGTTAACTTTTGTTCCTTAAGATGAAGACATGGTGATAGTACCG 665
Db	1137	GAGGAUUAUCAUCAGUCAUUAUACUGUUUCCCAAAUAGAGGAUAUGGUCAUGUACCA 1196
Qy	666	CTGTTTGAGGTTCTTATACAGCAAAAGATGACAGGAGTGAGGTCAATGTTAATCGT 725
Db	1197	UUUUCGACAUUUCUUUGGACUAGUAAAGAGGACGCGCAAGAGUUCUUAUGUGUCCAAG 1256
Qy	726	GACTTCGTTTACAGCTCTTAATCATATCAGAAATATCAAGCCAAAGCGCTTAACTTAC 785
Db	1257	GAUUUGUUUAUACUGUCUUAACCAUUCGACAAUACAGGCGGAGGCUUAUACAUAC 1316
Qy	786	CAGAACGTAATATCTTTCGTGAGTCTATATAAGATCCCGCGTGATAATCAATGGTGTACT 845
Db	1317	GCAAAUGUUUUGUCCUUUGUGGAAUUCGAUUCGAUGGAGGUUAUCAUUAACGUGUGACA 1376
Qy	846	GCTAGGTCGTAATGGGATGATAAAGCAATCTTCAACCCCTGTCAATGACTTTCTTC 905

Db	1377	GCAGGUCCGAUUGGGAUGGACAAACUUGUUAACAUCUUGUCCAUAGCAGCUUUAUC 1436
Qy	906	TTGCAGACTAAGCTGGCTGCGCTTCAAGACGATATAGTAATGGAAGATTTGCGTGTG 965
Db	1437	CUGCAUACUAAAGCUGCGCUUUAAGGAUGACUUAUCUGAUAGCAAGUUUAGUCUGGU 1496
Qy	966	GATAAGACCACTTCTGACTTATTTGGGATGAGGTGGGCAATTTTTCGAAAGCTTTTC 1025
Db	1497	UCGAAACCGGUGGCCAGCAUGUGUGAUGAUAUUCGUGCGUUUUUGGAAACGCAUUU 1556
Qy	1026	CCCACTATCAAGAGAGATTTGGTGAGCAGGAAAATCTCGATGTAACTGAGATGCTCTG 1085
Db	1557	CCUCCUGAAGAGAGGCUUUGAACAGGAAACUUAUCAGAGUGGCGAGCGCAUAU 1616
Qy	1086	AAGATCAAGATCCAGATCTGTATGTCAATGGAAGACAGGTTCTGTAGTGAATACACC 1145
Db	1617	GAGAUCAAGGGGCGUGAUCAUAUUGACCCUUCACACAGAUUAGUGACUGAGUACAAG 1676
Qy	1146	AAGTCTGAGGAGTTACCGCATCTAGATATCAAGAGGACTTAGAAGAGCTTGACCAATG 1205
Db	1677	GCUCUGUGACAUUGCCGCUUGACAUUAGGAAGAAUGGAAAGAAACGGAAGUGAUG 1736
Qy	1206	TACGACGCTTATCAGAAATTTATCTCTTAAAGGGTCTGATATATTTTCGATATCGCGAAG 1265
Db	1737	UACAAUGCAUUUCAGAGUUUCGGUGUUAAGGAGUCUGACAAAUUCGAUUGUAGUU 1796
Qy	1266	TTCAAAGACATGTGCAAGGCTTTAGATGTTAGTCTCTGATGTGGCAGCACGAGTAAATCGTT 1325
Db	1797	UUUCCAGAUUGGCCAAUCUUGGAAGUUGACCCAAUGACGCGCAGCGAAAGUUUAGUC 1856
Qy	1326	GCAGTGGCCGAGATAGAGGGTTTAACTTCTTACTTTTGTATAGCCAAACGAGGAGAT 1385
Db	1857	GCUGUCAUGAGCAUAGAGAGCGGUCUGACUCUCAUUUGAAACGACCUACUGAGCGCAU 1916
Qy	1386	GTGGCTAAGCTCT-----TAAAGCAGCGCGTCTGAGCGCGTGTATGTCTTGAACCG 1439
Db	1917	GUUGCGCUAGCUUUAACAGGAUCAGAGAGCGUUCUAGAGGUGCUUUGUAGUUAUCUUA 1976
Qy	1440	ACATCCGAGAGGTGAACGTPAAATTAATTTTCTATTCTCTGAGAAAGGAGGATTCCTGTG 1499
Db	1977	AGAGAGUUGAAGAAACCGUCCAUAGAGGUGUUGAUGCCAGAGGAGAGUUAACAAUAGCU 2036
Qy	1500	TGTGCAGAAATGATGTTTGAAGAATGCTAACTTAGACACCGAGGATTTGGAGTCCCTC 1559
Db	2037	GGUUCUGGAGAUCAUCGAGUGUCUUCUAUUCGAAACCGAGGAGUAGAGUUCUUUA 2096
Qy	1560	AACGATTTCCATAAGGCTTCGCTGGATAGTGTGATTACAAGCAAAATGGCATCGGTTGTC 1619
Db	2097	GAGCAUUUUAUAGGCAACCGGCAGAUUCGUUAAUUCGUAAGCAGAGAGGCUCCAUUGUG 2156
Qy	1620	TACACTGGCTCACTCAAAGTTCAAATAAGTAACTATGTGGAACAGTTTGGCAGCTTCG 1679
Db	2157	UACACGGGUCGUAUAAAGUUCAGCAAAUGAAAAACUUUAUCCGAVAGCCUGGUAAGCAUCA 2216
Qy	1680	TTGTCCGCCACTGTATCAAAATCTATGCAAGTCTCTAAAGGATGAAGTCGGGTATGATTCT 1739
Db	2217	CUAUCUGCGGUGUGCAUUCUGCUCAAGAUCCUCAAAGAUACAGCUGCUUUAUAGCCUU 2276
Qy	1740	GATTCCAGGAGAGAAAGTTGGTGTGTTGGGATGTCTACTTTGAAAAAGTGGCTCTCTCAACCT 1799
Db	2277	GAAACCCGCUCAAAGUUUGAGUUCUUGAUUGUUCAUUAGGAGAGUUGUUAUACAACCA 2336
Qy	1800	CGGCCAAAAGGTCAATCATGGGAGTTGTCTGTGATTTCAAGGGGAAAATGTTTACTGCA 1859
Db	2337	ACGCCAAGAGUCAUCAUGGGGUGUUUGAAAAACCCACGCGAGGAAGUAUCAUGUGGCG 2396
Qy	1860	CTTCTATCTTATGAAGGAGATAGATGCTGACTGAGAGCGACTGGAGAGGTCGCTGTA 1919
Db	2397	UUUUUGAAUAGUAGACAGGAGGUGUGUGACUUGCAUGAUUGGGAAGAGUAGUGUCUC 2456
Qy	1920	TCATCTGATACAAATGGTATATCTTGTATTTGCAAGCTTCCAAAATCTGAGGAAACATG 1979
Db	2457	AGCUCUGAGUCUGUUUUUAUCCGACAUUGCGGAAACUCAGAACTUCUGCGCAGACUGCU 2516

Db 4677 UUGAUCUGCAAAACUUGGUGUUAACACAUCAAGAUUGGGAACACUUGGAGGAGUUCAGAGA 4736
Qy 4188 GTGCTTTTGTGCGATGTTGCTTGTTCGCTCGGAACCTGGTCTTCTAGGCTTTCCCGACGCTG 4247
Db 4737 AGGUCUCUUGGAGUUGGUGUUCGU---GAACAAUUGCGUAUAACACACAGUUG 4793
Qy 4248 AACGAGGTATCAAGAGGTTTCATAAAACCGCGATGATGTTGTTGCTTTTAAATGT 4307
Db 4794 GACGACGUGAUGGAGGAGUUAUAGAACCGCCGCCUCCAGGUGGUGUUAUAAAGU 4853
Qy 4308 GTTAACAAATTTTGTGTGAATAATTTTATTTAGAACTTGTGTTTAAATGGCTGTAG 4367
Db 4854 CUGGUGAUAUUGGUGUUAUAGGAGGUGUUAUAGGAGGUGUUAUAGGUGGUGUUAU 4913
Qy 4368 TCTCAGAGATCTGTCAAATTTAGCGATTCATTCATCTTTTCGAAACAGGATGAGATACT 4427
Db 4914 UGUUAAAGGAAAGAGUUAUAGUUAUAGGUGUUAUAGGAGGAGGAGGAGGAGGAGGAG 4973
Qy 4428 TCCGCGATTCATGACTAAGGTCAAGAGTGTAGAAATATCGACTGTGCAACAGATATGGC 4487
Db 4974 ACCGUGAUGUUAACCCGUGAAGAGGUGUUAUAGGUGUUAUAGGAGGAGGAGGAGGAGG 5033
Qy 4488 TGTTAAGAAATGATGCTTTCTGATGTAGATTTTAAAGTGTAAAGTGTAGTTAAGAA 4547
Db 5034 UCAUGAAGAGUUAUAGGUGUUAUAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5093
Qy 4548 AGGCTATGCTGTGCTTGTAGTGTGCTGCGGAGTGAATCTCCCGGATACTG 4607
Db 5094 UGGAUACGUGUUAUGCGGUGUUGGUGUUAUAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5153
Qy 4608 CCGTGGTGTGCTGATGTTGTTATGTATGATGATGATGATGATGATGATGATGATGATGAT 4667
Db 5154 CAGAGGAGGUGAGGCGUGUGUGUGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUG 5213
Qy 4668 GCTGGTGGCTGATCAGCCCTGCTGCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4727
Db 5214 UCUGGAGUUAUACACAGAGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUG 5273
Qy 4728 TTATTCAATACATCCGAGGATGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4787
Db 5274 UUAUGCUAUAACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5333
Qy 4788 AGGAGTGGCTATGGAAGAGGATGCTGCTTTATCTTTTGTGAGTGTGTTCAATTTGTGT 4847
Db 5334 AAUUGAGAGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUG 5393
Qy 4848 AGTACATAAATAATGTAAAGAGGTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4907
Db 5394 UGUUUAAGAAAUAAUAAUAAUAAUAAUAAUAAUAAUAAUAAUAAUAAUAAUAAUAAUAAU 5453
Qy 4908 CTCGCCAATGAACTCACTGAAAGGTTGTTGAGGAGGTTCTGTGATGAAGTACCAATGGC 4967
Db 5454 AGGCCCAUGAAUUAUAAUAAUAAUAAUAAUAAUAAUAAUAAUAAUAAUAAUAAUAAU 5513
Qy 4968 TGTGA 4972
Db 5514 GAUCA 5518

RESULT 14
US-09-962-527-3
Sequence 3, Application US/09962527
Patent No. 6740740
GENERAL INFORMATION:
APPLICANT: GARGER, STEPHEN
HOLTZ, R. BARRY
MCCULLOCH, MICHAEL
TURPEN, THOMAS
TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
FROM PLANT SOURCES
NUMBER OF SEQUENCES: 5

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Howrey & Simon
;; STREET: 1299 Pennsylvania Avenue N.W.
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20004
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/962,527
;; FILING DATE: 24-Sep-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/037,751
;; FILING DATE: 10-march-1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Halluin, Albert P
;; REGISTRATION NUMBER: 25,277
;; REFERENCE/DOCKET NUMBER: 00801.0140.999
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-463-8109
;; TELEFAX: 650-463-8400
;; TELEX: <Unknown>
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6425 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: Genomic RNA
;; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-962-527-3

Query Match 40.8%; Score 2031; DB 4; Length 6425;
Best Local Similarity 44.4%; Pred. No. 0;
Matches 2212; Conservative 957; Mismatches 1795; Indels 21; Gaps 4;

Qy 6 AAGCTAATTCCTGAGTTTCAAGGGAGGCTTTTAAACAGGTATGACAGAGCTCCCAACGAA 65
Db 537 AAAACAGUCCCAACUCCCAAAAGAGCAUUAUGACAGUACGCGAGAAUUCUGAAGAC 596
Qy 66 GTCTGCTGCTCTAAACCTTTTCAGGATGTTCGAATACATCCGCCAGAGAAATAGTGGTAGA 125
Db 597 GCUGUCUGACAAUUAUCCAGACAAUUGCGACAUUGCGAGCAUUGCAGCAUUGCAGGAGA 656
Qy 126 AGATACGCTGTTGCTGCGACAGTTTGTATGATATTCCTGTGCAATGATGTTTGGAGCTGCG 185
Db 657 GUGUAGUCCAUUGCGUACACAGCAUAUAGCAUACAGCCGCAUAGUUGCGGCGGCA 716
Qy 186 TTAATATCTAAGATATACATGATGTATGTCAGCTTCCATTTTGGCAGAGCATTATTA 245
Db 717 CUCUUGAGGAGAAAUUGUCCAUUGCGUCCUUCUCCUUCUUCUUGAGAACCUUGCU 776
Qy 246 CTAGACCAGACGGAGTTACGCTTAATGAATAGCGCAACTTTTCAAAAGAGAGAGGTGAT 305
Db 777 CUUGAAGAUCAUACGUCAUUAUUGGACGAGAAUACACGCGUGUUUUUCGCGGAGAGAC 836
Qy 306 GATGTTTCTTTTCTTTGCTGATGAAGTACTTTAAATATTAGTCAATAATACAAAAT 365
Db 837 AAGUAGACCUUUUUGCAUACAGAGAGUACUUAUUAUUGUUAUUGUUAUUGUUAUUG 896
Qy 366 ATCTTGCAATTATGTAGTTAAATCTTACTTTCTGCTCTCTAGTAGAATAGTTTACTTAAAG 425
Db 897 AUUCUUAAGUAGUGUGCAAAAACUUAUUCGCGCCUUAUAGAGAGGUGUUAUAGUAG 956
Qy 426 GAATTTTACTGCTAGGTTAAATTAATTAATTTGTTAAATTTTACCAAGTAGATACCTAT 485
Db 957 GAGUUUUAUGACACAGAGUUAUACUGGUGUUUUGUUAUUGUUAUUGUUAUUGUUAUUG 1016

QY 1206 TAGACGCGTTATCAGAAATTATCTATCCTTAAAGGTCCTGATTAATTTTCGATATCGCGAAG 1265
D 1737 UACAAGCAUUUCAGAGUAUUCGGUGUAUAGGAGUCUGACAAUUCGAUUGUAUGUU 1796
QY 1266 TTCAAGACATGTCCAAAGGCTTTAGATTAGTTCCTGATGTGGCAGCAGCAGTAATCGTT 1325
D 1797 UUUUCCAGAUUGCCAAUCUUUUGAAGUUGACCAAGAGCGAGCGAAGGUUAUAGUC 1856
QY 1326 GCAATGCGCCGAGATAAGAGCGGTTAACTCTTACTTTTATTAAGCCAAACCGAGGAAT 1385
D 1857 GCGUCAUGAGCAUGAGAGCGGUCUGACUCUCAUUUGAAACGACCUACUGAGCGGAU 1916
QY 1386 GTGCGTAAGGCTCT-----TAAAGCACGCGCTCTGAGCGCGTGTATGTCTTGAACCG 1439
D 1917 GUUGCGUAGCUUUAACAGGAUCAAGAGAGGCUUCAAGAGGUGCUUUGUAGUUAUCUCA 1976
QY 1440 ACATCCGAAGAGGTGAACGTAATAATTTCTATGCTGAGAAAGGAGATTGCCCTGTG 1499
D 1977 AGAGAAGUAGNAAGCCGUCUAGNAGGUGUUGAGGCCAGAGGAGAGUUAUACAUAUGCU 2036
QY 1500 TGTGCAGAAAGTCATGTTTGAACGAATGCTAACTTAGAGCACCAAGGAGTTGGAGTCCCTC 1559
D 2037 GGUCUUGCGAGAUCAUCCGAGUCGUCUUAUUAAGAACGAGGAGUAGAGUCUUUA 2096
QY 1560 AACGATTTCCATAGGCTTGGTGGATGTGTGATTACAAGCAAAATGGCATCGGTGTC 1619
D 2097 GAGCAGUUUAUUGGCAACGCGCAGAUUCGUUAUUCGUAAGCAGAGAGCUCGUAUUG 2156
QY 1620 TACACTGCTCAGCTCAAGTTTCAACAAATGAAGAACTATGTGGACAGTTTGGCAGCTTCG 1679
D 2157 UACACGGGUCGUAUUAAGUUCACAAUAGNAACUUUAUCUAUAGCCUUGUAGCAUCA 2216
QY 1680 TTGTCGCCACTGTATCAAACTTATGCAAGTCACTAAAGGATGAAGTCGGGTATGATTC 1739
D 2217 CUUUCUGCGGUGUGAUCUCUCAAGAUCCUCAAGAUACAGCUGCUUUAUGACCU 2276
QY 1740 GATTCAGGAGAAAGTTGGTTTGGATGCTCACTTTGAAAGAGTGGCTCCTCAAACT 1799
D 2277 GAAACCCGCUAAAAGUUGGAGUCUUGGAUUGUUGAUCUAGGAAGUGGUUAUCAAACCA 2336
QY 1800 GCGGCCAAAGTCATTATGCGGAGTTGTCTGATTTACAAGGGGAAATGTTTACTTGCA 1859
D 2337 ACGGCCAAGAGUCAUGGCGGUGUUGUUAACCCAGCGAGAGUAUAGUUGGCG 2396
QY 1860 CTTCTATCTTATGAAGAGATAGAAATGCTGATCGAGAGCGACTGGAGAGGTTGCTGTA 1919
D 2397 CUUUGGAAUUAUGAGAGCGGUGUGACUUGCGAUGCAUGCAUUGGAGAGUAGUCUG 2456
QY 1920 TCATCTGATCAATGTTATTTCTGATATTGCAAGCTCCAAAGCTCAGGAAACATG 1979
D 2457 AGCUCUGAGUCUGUUUAUUCGACAUGCGGAAACUCAGAACUCUGCGCAGACUGCU 2516
QY 1980 AGAGCGGTGAACCCCGAACCTTACTGCAAGATGTTGATGTTGGATGGGTCCTGGT 2039
D 2517 CGAAACGGAGAACCGCAUGACUAGCGCAAGGUGUUGUUGGAGCGAGUUCGCGC 2576
QY 2040 TGTGGAAGTACAAGAGGATTTTGAAGATTTGATCTTGTATGAGGATTTGATCTTGTT 2099
D 2577 UUGGGGAAACCAAGAAAUUUUUUCCAGGGUUAUUUUGAAGAAUCUAUUUUAGUA 2636
QY 2100 CTTGGAACCAAGCTGCTGCTATGATCAGAGAGGCTTAATTCATCTGGACTGATAGA 2159
D 2637 CCUGGGAAGCAAGCGCGGAAUAGCAUAGAGAGCGUGGCAAUUCUCAGGGAUUUUG 2696
QY 2160 GCCAATATGGAACAATGTGAGAACGATAGATTCACTTCTAATGCAAT-----CCAAA 2210
D 2697 GCCAGAGAGCAACACUUAAACCGUUGAUUUUUAUGAUGAAUUUUGGAAAGACACA 2756
QY 2211 CCGCGATCACAACAAGAGCTTTTATGATGAAGAGTTGATGCTGCAACCGGTTGTT 2270
D 2757 CGCUGCAGUUAACAAGAGGUUAUUAUGAAGAGGUGUUGAUGUUGCAUACUGGUGUGU 2816
QY 2271 AACTTCCTGGTCTATCTCTGTTGCGACATCGCATACATTTTACAGATCTGCGCGCATC 2330

D 2817 AUUUUUCUGGCGAUGUUAUUGCGGAAAUUGCAUUAUUGCGGAGACACACAGCAG 2876
QY 2331 ATTCTCTTCAATTAACAGAGTTTCAAAATTTCCGTATCCCAAAATTTTGAGAGCTGCAA 2390
D 2877 AUUCAUAACAUAUAGUUCAGGAUUCGCCGUAUCCCGCCCAUUUUGCCAAUUGGAA 2936
QY 2391 GTGGATGAAGTTGAGATGAGGAGGACCACTAGATGAGTCCAGGTGATGTAATTTTC 2450
D 2937 GUUGACGAGGUGAGACACGAGAACUACUCUCGUGUCCAGCGGCAUGUACACAUU 2996
QY 2451 CTACAATCGAAGTACGAAGGAGCGGTGACAAACCACTTCAACTGTACAACTCGTCTCA 2510
D 2997 CUGAACAGGAGUAUAGAGGCUUUGAUGAGCACAUCUUCGUGUUAUAAAGUCUGUUG 3056
QY 2511 TCTGAGATGATAGCGGTAAAGGAGTACTAAACAGTGTTCCTCAAAACCACTAAAGGAAA 2570
D 3057 CAGGAGUGGCGCGGAGCGCGUGAUCAUCCGAGUACAAACCCUUGCAUGGCAAG 3116
QY 2571 ATTGTAATCTTCACTCAGGCTGATAAATTTGAGTTAGAGGAGAGGCTATAGAAATGTG 2630
D 3117 AUCUCGACUUUUAUCCCAUCCGAAUAAAGAGAGCUCUGCUUUAAGAGGUAUUCAGAU 3176
QY 2631 AACACGTTTCATGAGATCCAAGGAGAAACCTTTGAAGATGTCGCTGTCAGATTCAAG 2690
D 3177 CACACUGUGAUGAUGGCAAGGAGAGACAUACUCUGAUGUUAUUAUAGUUAUUAAC 3236
QY 2691 GCAACTCCACTGACTCTGATTTTCCAAAGTCTTCCCGCATGTTCTAGTCGCTGACTAGA 2750
D 3237 CCUACACAGCUCUUAUUGCAGGAGACAGCCCAUGUUGGCGCAUUGUCAAAG 3296
QY 2751 CACAAAAGAGCTTCAAAATTTACACGTTAGTTAGATCTTTAGTACAGATAATTTAGT 2810
D 3297 CACACCUUGGCGUCAAGUACACUCUGUUGUUAUGAUCUUAUUGUAGUUAUUAUGA 3356
QY 2811 GATTGTCTTCTTTTAAAGTCTCTTTTAAAGATGTATATGTTAGAAAGCAGGTAGTAGA 2870
D 3357 GAUCUAGAGAAACUUAAGCUCUUAUUGUUAUUAUUAUUAUUAUUAUUAUUAUUA 3416
QY 2871 TAGCAATTAACAGATGAGTGTGTTCAAAAGGTGATAATCTCTTTGTTGGCAACCTAAA 2930
D 3417 UAGCAUUAACAGAUAGACUCGUGUCAAAGGUAUCCAAUUCUUAUUGGCGAGCCCAAAG 3476
QY 2931 TCAGGAGACTTTCCAGATCTACAGTTCTATTACGATGTATGCTCCTCGCTGATAGTACT 2990
D 3477 ACUGGUAUUAUUCUGAUAUGCAGUUUAUUAUGAUAUGUGUCCCGAGCAACAGCACC 3536
QY 2991 ATACTTAAAGATGATGCTGTTTACCATGAGTTACGTGATATAGTCTTAAATGTGAAG 3050
D 3537 AUGAUAUAUUAUUAUGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3596
QY 3051 GATTGTGTTCTTGATTTTCCAAAAGTATTTCCGATGCCAAGAGGTTGAAACCATGCTA 3110
D 3597 GAUUGCAUUAUUGAUAUUGCUAAGUCUGUUGCGCUAAGGAUCAAUUAUUAUUAUUA 3656
QY 3111 GAGCAGTTTGTGTCACCGCGCGGACCGCCAGGCTCGAGACTACTCGAAAATCTG 3170
D 3657 AUACCUAUGUACGAAACGCGCGGAGAAUUGCCAGCGCAGACUGGACUUAUUGGAAAUUA 3716
QY 3171 GTTGCATATGATTAAGAAATTTCAACGCAACAGACTGACGGGAGCGATTGACATTTGAG 3230
D 3717 GUGCGAUAUUAUUAAGAAACUUAUUAAGCAACCCGAGUUGUUGGCAUCAUUAUUAUUA 3776
QY 3231 AGCACCGCATCTGTTGATGATAAGTTTTTTTGTAGTATTTTATTAATAAAGAAAAA 3290
D 3777 AAUACUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3836
QY 3291 TACAAAAAATATTCGTGAGTGTATGACGAGGATTCATGATGATGATGATGATGATGAT 3350
D 3837 AAACCAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3896
QY 3351 AGGAAAGAGTACTATTTGGACGACTTGGCTAACTTACAAATTTTACAGATCTGCGCGCATC 3410

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 28, 2005, 08:33:34 ; Search time 1883.98 Seconds
(without alignments)

17081.170 Million cell updates/sec

Title: US-09-551-494-5_COPY_534_5505

Perfect score: 4972

Sequence: 1 ctaacaggaattctctgag.....tgaagtaacaaatgggtgtga 4972

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:**

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4972	100.0	6355	15	US-10-321-434-7
2	2034.2	40.9	6395	10	US-09-962-527-1
3	2034.2	40.9	6395	19	US-10-828-029-1
4	2034.2	40.9	6439	10	US-09-962-527-2
5	2034.2	40.9	6439	19	US-10-828-029-2
6	2031	40.8	6395	17	US-10-338-592-2
7	2031	40.8	6425	10	US-09-962-527-3

RESULT 1
US-10-321-434-7
; Sequence 7, Application US/10321434
; Publication No. US20030135882A1
; GENERAL INFORMATION:
; APPLICANT: Metzlaff, Michael
; APPLICANT: Meulewater, Frank
; APPLICANT: Gossel, Veronique
; APPLICANT: Fach, Ina
; TITLE OF INVENTION: Improved methods and means for delivering inhibitory RNA to plants
; TITLE OF INVENTION: applications thereof
; FILE REFERENCE: FKOMOD
; CURRENT APPLICATION NUMBER: US/10/321.434
; CURRENT FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 6355
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: cDNA sequence of the genome of TMV-U2
US-10-321-434-7

ALIGNMENTS

8	2031	40.8	6425	19	US-10-828-029-3	Sequence 3, Appli
9	2031	40.8	6446	10	US-09-962-527-5	Sequence 5, Appli
10	2031	40.8	6446	19	US-10-828-029-5	Sequence 5, Appli
11	2031	40.8	6475	10	US-09-962-527-4	Sequence 4, Appli
12	2031	40.8	6475	19	US-10-828-029-4	Sequence 4, Appli
13	2031	40.8	10600	16	US-10-356-708-1	Sequence 1, Appli
14	2031	40.8	10600	19	US-10-280-913A-1	Sequence 1, Appli
15	2031	40.8	10600	19	US-10-684-134-1	Sequence 1, Appli
16	2031	40.8	10600	19	US-10-637-758-1	Sequence 1, Appli
17	2031	40.8	10624	16	US-10-356-708-2	Sequence 2, Appli
18	2031	40.8	10624	19	US-10-280-913A-2	Sequence 2, Appli
19	2031	40.8	10624	19	US-10-684-134-2	Sequence 2, Appli
20	2031	40.8	10624	19	US-10-637-758-2	Sequence 2, Appli
21	2031	40.8	11222	19	US-10-679-620-73	Sequence 73, Appli
22	2031	40.8	11641	9	US-09-993-059-33	Sequence 33, Appli
23	2031	40.8	11641	15	US-10-103-327-33	Sequence 33, Appli
24	2031	40.8	11641	18	US-10-684-300-13	Sequence 13, Appli
25	2031	40.8	11641	18	US-10-684-349-13	Sequence 13, Appli
26	2031	40.8	11641	20	US-10-851-388-33	Sequence 33, Appli
27	2031	40.8	11641	22	US-10-984-389-33	Sequence 33, Appli
28	2029.4	40.8	7685	9	US-09-949-317-22	Sequence 22, Appli
29	2029.4	40.8	7685	9	US-09-949-317-25	Sequence 25, Appli
30	2029.4	40.8	7685	9	US-09-949-316-22	Sequence 22, Appli
31	2029.4	40.8	7685	9	US-09-949-316-25	Sequence 25, Appli
32	2029.4	40.8	7685	14	US-10-200-051-22	Sequence 22, Appli
33	2029.4	40.8	7685	14	US-10-200-051-25	Sequence 25, Appli
34	2029.4	40.8	7686	9	US-09-949-317-23	Sequence 23, Appli
35	2029.4	40.8	7686	9	US-09-949-316-23	Sequence 23, Appli
36	2029.4	40.8	7686	14	US-10-200-051-23	Sequence 23, Appli
37	2029.4	40.8	7687	9	US-09-949-317-24	Sequence 24, Appli
38	2029.4	40.8	7687	9	US-09-949-316-24	Sequence 24, Appli
39	2029.4	40.8	7687	14	US-10-200-051-24	Sequence 24, Appli
40	2029.4	40.8	7688	9	US-09-949-317-27	Sequence 27, Appli
41	2029.4	40.8	7688	9	US-09-949-316-27	Sequence 27, Appli
42	2029.4	40.8	7688	14	US-10-200-051-27	Sequence 27, Appli
43	2029.4	40.8	10132	9	US-09-978-199-3	Sequence 3, Appli
44	2027.8	40.8	10607	16	US-10-098-155-1	Sequence 1, Appli
45	2027.8	40.8	10631	16	US-10-098-155-2	Sequence 2, Appli

Query Match 100.0%; Score 4972; DB 15; Length 6355;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTACAAAGTAACTTCCTGAGTTTCAAGGGAGGCTTTTAAACAGGTATCGAGAGCTCCCA 60

Db 534 CTAACAAGGTAATTCCTGAGTTTCAAAGGGAGGCTTTTAAACAGGTATGCGAAGCTCCCA 593
Qy 61 ACGAAGTCTGCTCTAAACATTTTTCAGGATTTGTCGAATATACATCCGCCAGAGAAATAGTG 120
Db 594 ACGAAGTCTGCTCTAAACATTTTTCAGGATTTGTCGAATATACATCCGCCAGAGAAATAGTG 653
Qy 121 GTAGAAGATACGCTGTGCTCTGACAGATTTGTAATGATATTCCTGTGCGATGAGTTTGGAG 180
Db 654 GTAGAAGATACGCTGTGCTCTGACAGATTTGTAATGATATTCCTGTGCGATGAGTTTGGAG 713
Qy 181 CTGCGTTAAATCTTAAGAATATACATGTATGTTATGAGCTTCCATTTTTCGCGAAGCAT 240
Db 714 CTGCGTTAAATCTTAAGAATATACATGTATGTTATGAGCTTCCATTTTTCGCGAAGCAT 773
Qy 241 TATTACTAGACAGACGAGGTTTACGCTTAATGAATAGGCGCAACTTTCAAAGAGAAAG 300
Db 774 TATTACTAGACAGACGAGGTTTACGCTTAATGAATAGGCGCAACTTTCAAAGAGAAAG 833
Qy 301 GTGATGATGTTTCTTTTCTTCTGCTGATGAAGTACTTTAAATATATAGTCATAAATACA 360
Db 834 GTGATGATGTTTCTTTTCTTCTGCTGATGAAGTACTTTAAATATATAGTCATAAATACA 893
Qy 361 AAAATATCTTGCAATATAGTAAATCTTACTTTCTGCTTCTAGTAGAATAGTTTACT 420
Db 894 AAAATATCTTGCAATATAGTAAATCTTACTTTCTGCTTCTAGTAGAATAGTTTACT 953
Qy 421 TTAAGGAATTTTATAGTCACTAGGTTTAAATCTTGGTTTGTAAATTTTACCAAAAGTAGATA 480
Db 954 TTAAGGAATTTTATAGTCACTAGGTTTAAATCTTGGTTTGTAAATTTTACCAAAAGTAGATA 1013
Qy 481 CCTATATCTGTACAAGATGTTAGACAAGTAGGTTGTGATAGTATGATCAGTTCTATGAGG 540
Db 1014 CCTATATCTGTACAAGATGTTAGACAAGTAGGTTGTGATAGTATGATCAGTTCTATGAGG 1073
Qy 541 CGATGGAAGACGCTTTCCTTACAAAGAAACCTTGGCCATGTTTCAACACTGAAGAGCAA 600
Db 1074 CGATGGAAGACGCTTTCCTTACAAAGAAACCTTGGCCATGTTTCAACACTGAAGAGCAA 1133
Qy 601 TCTTTAGAGACACGCGTTTCGTTTAACTTTTGGTTTCCCTTAAGATCAAGGACATGTTGATAG 660
Db 1134 TCTTTAGAGACACGCGTTTCGTTTAACTTTTGGTTTCCCTTAAGATCAAGGACATGTTGATAG 1193
Qy 661 TACCGTGTGAGGGTTCTAATACAGCAAAAAGATGACAAGGAGTGAAGTCAATGTTA 720
Db 1194 TACCGTGTGAGGGTTCTAATACAGCAAAAAGATGACAAGGAGTGAAGTCAATGTTA 1253
Qy 721 ATCGTGACTTCGTTTACACAGTGTCTAATCATATCAGAACATATCAAGCCAAAGCGTTAA 780
Db 1254 ATCGTGACTTCGTTTACACAGTGTCTAATCATATCAGAACATATCAAGCCAAAGCGTTAA 1313
Qy 781 CTTACCAAGACGTATTATCTTTCTGAGGTCCTAATAGATCCCGGTGATATCAATGGTG 840
Db 1314 CTTACCAAGACGTATTATCTTTCTGAGGTCCTAATAGATCCCGGTGATATCAATGGTG 1373
Qy 841 TTACTGTAGTCTGAATGGGATGATATAAGCAATTTCTTCAACCCCTTGTCAATGACTT 900
Db 1374 TTACTGTAGTCTGAATGGGATGATATAAGCAATTTCTTCAACCCCTTGTCAATGACTT 1433
Qy 901 TCTTCTTGACACTAAGCTGCGCTTCAAGACGATATAGTAATCGGAAGTTTTCGGT 960
Db 1434 TCTTCTTGACACTAAGCTGCGCTTCAAGACGATATAGTAATCGGAAGTTTTCGGT 1493
Qy 961 GCTTGGATAGACCACTTCTGAACCTTATTTGGGATGAGTGGGCAAAATTTTTCGAAACG 1020
Db 1494 GCTTGGATAGACCACTTCTGAACCTTATTTGGGATGAGTGGGCAAAATTTTTCGAAACG 1553
Qy 1021 TTTTCCCACTATCAAGAGAGATGTTGTGACAGCAAAAATTTCTGATGTAAGTGAGAAATG 1080
Db 1554 TTTTCCCACTATCAAGAGAGATGTTGTGACAGCAAAAATTTCTGATGTAAGTGAGAAATG 1613
Qy 1081 CTCTGAAGATCAAGATCCAGATCTGTATGTACATGGAAGACAGGTTTCGTAGCTGAAT 1140
Db 1614 CTCTGAAGATCAAGATCCAGATCTGTATGTACATGGAAGACAGGTTTCGTAGCTGAAT 1673

Qy 1141 ACACCAAGTCTGAGGAGTTTACCOCATCTAGATATCAAGAAGGACTTTAGAAAGAGCTGAGC 1200
Db 1674 ACACCAAGTCTGAGGAGTTTACCOCATCTAGATATCAAGAAGGACTTTAGAAAGAGCTGAGC 1733
Qy 1201 AAATGTACGACGCGTTTATCAGAAATTTATCTTAAAGGCTGCTGATAAATTTTCGATATCG 1260
Db 1734 AAATGTACGACGCGTTTATCAGAAATTTATCTTAAAGGCTGCTGATAAATTTTCGATATCG 1793
Qy 1261 CGAAGTTCAAAGACATGTGCAAGGCTTTAGATGTTAGTCTCTGATGTGGCAGCAGAGTAA 1320
Db 1794 CGAAGTTCAAAGACATGTGCAAGGCTTTAGATGTTAGTCTCTGATGTGGCAGCAGAGTAA 1853
Qy 1321 TCGTGTCAGTGGCGGAATAGAAAGCGGTTTAACTCTTACTTTTGATGAAGCAACCGAGG 1380
Db 1854 TCGTGTCAGTGGCGGAATAGAAAGCGGTTTAACTCTCTTACTTTTGAAGCAACCGAGG 1913
Qy 1381 AGAATGTGCTAAGGCTCTTAAAGCACCGGCTCTGAGGCGGTGATGTTGTTGAACCGA 1440
Db 1914 AGAATGTGCTAAGGCTCTTAAAGCACCGGCTCTGAGGCGGTGATGTTGTTGAACCGA 1973
Qy 1441 CATCCGAAGAGGTGAACCTTAAATTTTCTATTTGCTGAGAAAGGGAGATTGCTCTGTG 1500
Db 1974 CATCCGAAGAGGTGAACCTTAAATTTTCTATTTGCTGAGAAAGGGAGATTGCTCTGTG 2033
Qy 1501 GTGCAGAAAGTCATGTTTGAACGAAATGCTAACTTTAGAGCAACGAGGATTGGAGTCCCTCA 1560
Db 2034 GTGCAGAAAGTCATGTTTGAACGAAATGCTAACTTTAGAGCAACGAGGATTGGAGTCCCTCA 2093
Qy 1561 ACATTTTCCATTAAGGCTTGGTGGATGTGATTAACAAGCAAAATGGCATCGGTTCTCT 1620
Db 2094 ACATTTTCCATTAAGGCTTGGTGGATGTGATTAACAAGCAAAATGGCATCGGTTCTCT 2153
Qy 1621 ACATGCTCACTCAAAAGTTTCAACAAATGAAGAACTATGTGGACAGTTTGGCAGCTTCGT 1680
Db 2154 ACATGCTCACTCAAAAGTTTCAACAAATGAAGAACTATGTGGACAGTTTGGCAGCTTCGT 2213
Qy 1681 TGTCCGCACTGTATCAAAATCTATGCAAGTCACTAAAGGATGAAGTCCGGGTATGATCTG 1740
Db 2214 TGTCCGCACTGTATCAAAATCTATGCAAGTCACTAAAGGATGAAGTCCGGGTATGATCTG 2273
Qy 1741 ATTCCAGGGAAGATTTGGTGGATGCTCACTTTGAAAAGTGGCTCTCAAAACCTG 1800
Db 2274 ATTCCAGGGAAGATTTGGTGGATGCTCACTTTGAAAAGTGGCTCTCAAAACCTG 2333
Qy 1801 CGGCCAAAAGTCAATTCATGGGAGTTTCTCTGGAATTAACAAGGGGAAAATGTTTACTGCAC 1860
Db 2334 CGGCCAAAAGTCAATTCATGGGAGTTTCTCTGGAATTAACAAGGGGAAAATGTTTACTGCAC 2393
Qy 1861 TTCTATCTTATGAAGGAGATAGAAATGGTGACTGAGACGCACTGGAGAGGGTGGCTGTAT 1920
Db 2394 TTCTATCTTATGAAGGAGATAGAAATGGTGACTGAGACGCACTGGAGAGGGTGGCTGTAT 2453
Qy 1921 CATCTGATACAATGGTATATTTCTGATATTCGAAGCTTCAAAATCTCAGAGAAAACAATGA 1980
Db 2454 CATCTGATACAATGGTATATTTCTGATATTCGAAGCTTCAAAATCTCAGAGAAAACAATGA 2513
Qy 1981 GAGACGCTGAACCCCAACGAACTTCTCAAAAGATGGTACTTTGTGGATGGGGTGGCTGGTT 2040
Db 2514 GAGACGCTGAACCCCAACGAACTTCTCAAAAGATGGTACTTTGTGGATGGGGTGGCTGGTT 2573
Qy 2041 GTGAAAAGTACAAGGAGATTTTGAAGATTTGATCTTTGATGAGGATTTGATCTTGGTTC 2100
Db 2574 GTGAAAAGTACAAGGAGATTTTGAAGATTTGATCTTTGATGAGGATTTGATCTTGGTTC 2633
Qy 2101 CTGAAAACAGCTGCTGCTATGATCAGAAAGAGGGCTAATTCATCTGGACTGATAAGAG 2160
Db 2634 CTGAAAACAGCTGCTGCTATGATCAGAAAGAGGGCTAATTCATCTGGACTGATAAGAG 2693
Qy 2161 CCACAAATGGAACAATGTGAGAACCGGTAGATTCACTTCTAATGCAATCCAAAACCGCGATCAC 2220
Db 2694 CCACAAATGGAACAATGTGAGAACCGGTAGATTCACTTCTAATGCAATCCAAAACCGCGATCAC 2753

2221 QY ACAAGAGGCTTTTATTTGATGAAGGTTGATGCTGCACACCGGTTGTGTAACTTCTCTCG 2280
2754 Db ACAAGAGGCTTTTATTTGATGAAGGTTGATGCTGCACACCGGTTGTGTAACTTCTCTCG 2813
2281 QY TGCCTTATCTCTGTTTGGGATCGCATACATTTTACGGAGATACACAGCAGATTCCTTTTCA 2340
2814 Db TGCCTTATCTCTGTTTGGGATCGCATACATTTTACGGAGATACACAGCAGATTCCTTTTCA 2873
2341 QY TTAAACAGAGTTTCAAGAAATTTCCCGTATCCCAACATTTTGAAGAGCTGCAAGTGGAAGAAG 2400
2874 Db TTAAACAGAGTTTCAAGAAATTTCCCGTATCCCAACATTTTGAAGAGCTGCAAGTGGAAGAAG 2933
2401 QY TTGAGATGAGGAGGACACACCTGAGATGCCAGGTGATGTAATTTTTCCTACAATCGA 2460
2934 Db TTGAGATGAGGAGGACACACCTGAGATGCCAGGTGATGTAATTTTTCCTACAATCGA 2993
2461 QY AGTACGAGAGCGGTGACACACCTTCACTGTACAAACGATCGGTCTCATCTGAGATGA 2520
2994 Db AGTACGAGAGCGGTGACACACCTTCACTGTACAAACGATCGGTCTCATCTGAGATGA 3053
2521 QY TAGGCGGTAAAGGAGTAAACAGTGTTCCTAAACCCACTTAAAGGGAATTTGTAACCTT 2580
3054 Db TAGGCGGTAAAGGAGTAAACAGTGTTCCTAAACCCACTTAAAGGGAATTTGTAACCTT 3113
2581 QY TCACTCAGGCTGATAAAATTTGAGTTAGAGGAGAGGCTTATAAGAAATGTGAACACCGTTT 2640
3114 Db TCACTCAGGCTGATAAAATTTGAGTTAGAGGAGAGGCTTATAAGAAATGTGAACACCGTTT 3173
2641 QY ATGAGATCCAAGGAGAAACCTTTTGAAGATGTGCTGTGTCAGATTTGAACCGCACTCCAC 2700
3174 Db ATGAGATCCAAGGAGAAACCTTTTGAAGATGTGCTGTGTCAGATTTGAACCGCACTCCAC 3233
2701 QY TGAATCTGATTTCCAGTCTTCCCGCATGTTCTAGTCCGCTCTGACTAGACACACAAAGA 2760
3234 Db TGAATCTGATTTCCAGTCTTCCCGCATGTTCTAGTCCGCTCTGACTAGACACACAAAGA 3293
2761 QY GCTTTCAAAATTTACACCGTAGTGTAGATCTTTTGTAGTACAGATAAATTTAGTGTCTT 2820
3294 Db GCTTTCAAAATTTACACCGTAGTGTAGATCTTTTGTAGTACAGATAAATTTAGTGTCTT 3353
2821 QY CTTTAAAGCTCTTCTTTTGAAGATGTATATGTTAGAGAGGATGTAGATGATCAATTTAC 2880
3354 Db CTTTAAAGCTCTTCTTTTGAAGATGTATATGTTAGAGAGGATGTAGATGATCAATTTAC 3413
2881 QY AGATGATGACAGTGTTCAGAGTCTAATCTCTTTTGTGGCAACACCTTAATCAGGAGACT 2940
3414 Db AGATGATGACAGTGTTCAGAGTCTAATCTCTTTTGTGGCAACACCTTAATCAGGAGACT 3473
2941 QY TTCCAGATCTACAGTCTTATTTACGATGTATGCTCTCCCTGTTAATAGTACTATATCTTAA 3000
3474 Db TTCCAGATCTACAGTCTTATTTACGATGTATGCTCTCCCTGTTAATAGTACTATATCTTAA 3060
3001 QY AGTATGATGCTGTTACCATGAGTTACGTGATATAGTCTTAAATGTGAAGGATGTGTTT 3060
3534 Db AGTATGATGCTGTTACCATGAGTTACGTGATATAGTCTTAAATGTGAAGGATGTGTTT 3593
3061 QY TTGATTTTCCAAAAGTATTCGATGCCAAGAGGTTGAACCATGCTGTAGAGCCAGTTT 3120
3594 Db TTGATTTTCCAAAAGTATTCGATGCCAAGAGGTTGAACCATGCTGTAGAGCCAGTTT 3653
3121 QY TGGGTACCGGGCGGAAACCGGAGGCTGCAGGACTCTCGAATACTGTTGCAATGA 3180
3654 Db TGGGTACCGGGCGGAAACCGGAGGCTGCAGGACTCTCGAATACTGTTGCAATGA 3713
3181 QY TTAAAGAAATTTTCAACGACACAGCTGACGGGAGCATTTGACATTTGAGAGCACCGCAT 3240
3714 Db TTAAAGAAATTTTCAACGACACAGCTGACGGGAGCATTTGACATTTGAGAGCACCGCAT 3773
3241 QY CTGTTGATGATAGTATGTTTGTGATAGTATTTTATTAATAAGAAAAATACAAAAA 3300
3774 Db CTGTTGATGATAGTATGTTTGTGATAGTATTTTATTAATAAGAAAAATACAAAAA 3833
3301 QY ATATTGCTGGAGTGATGACGAGGATTCATGATGAGATGTTGGAACACAGGAAAGAAG 3360

3834 Db ATATTGCTGGAGTGATGACGAAAGGATTCATGATGAGATGGTTGGAACACAGGAAAGAAG 3893
3361 QY TACTATTGACGACTTGGCTAACTACAAATTTTACAGATCTGCGGCGCATCGATCAGTACA 3420
3894 Db TACTATTGACGACTTGGCTAACTACAAATTTTACAGATCTGCGGCGCATCGATCAGTACA 3953
3421 QY AGCAGATGATCAAGGCTCAACCAAAACAGAAATTTGAACCTTTCAATTCAGATGAATACC 3480
3954 Db AGCAGATGATCAAGGCTCAACCAAAACAGAAATTTGAACCTTTCAATTCAGATGAATACC 4013
3481 QY CTGCTCTGCAACCAATTTGCTACCATTTGCAAGCAGATCAACGGTATTTTGGCCGGTTCT 3540
4014 Db CTGCTCTGCAACCAATTTGCTACCATTTGCAAGCAGATCAACGGTATTTTGGCCGGTTCT 4073
3541 QY CAGAGCTTCAAGAGTTGCTCTGAGGCAATTTGATTTCTAAGAGATTTCTTTTCTTACTA 3600
4074 Db CAGAGCTTCAAGAGTTGCTCTGAGGCAATTTGATTTCTAAGAGATTTCTTTTCTTACTA 4133
3601 QY GGAAAACTCCAGAACAGATTTCAAGAAATTTTCTCGATCTCGACTCGACGTTCTCTATGG 3660
4134 Db GGAAAACTCCAGAACAGATTTCAAGAAATTTTCTCGATCTCGACTCGACGTTCTCTATGG 4193
3661 QY ATGTGTTAGAACTGATATTTCTAAGTATGATAAGTCAAGACGATTTTCAATGTGCTG 3720
4194 Db ATGTGTTAGAACTGATATTTCTAAGTATGATAAGTCAAGACGATTTTCAATGTGCTG 4253
3721 QY TAGAGTATCAAAATATGAAAAAGATTTGGGTCTCAATGAGTATTTTGGCCGGAAGTGTGAAAC 3780
4254 Db TAGAGTATCAAAATATGAAAAAGATTTGGGTCTCAATGAGTATTTTGGCCGGAAGTGTGAAAC 4313
3781 QY AAGGGCACAGGAAAAACCTTTGAAGATTTACATTTCTGGAATCAAGACATGTCTGTGGT 3840
4314 Db AAGGGCACAGGAAAAACCTTTGAAGATTTACATTTCTGGAATCAAGACATGTCTGTGGT 4373
3841 QY ATCAAGAGAAAAACCGGTGATGTGACTACTTTTCAATCGCAATCTGTTTATTAATAGCAGCTT 3900
4374 Db ATCAAGAGAAAAACCGGTGATGTGACTACTTTTCAATCGCAATCTGTTTATTAATAGCAGCTT 4433
3901 QY GCTTGGGTTCAATGTTTACCGATGAAAAAGGTCAATAAAGGTGCTTTTGTGGAGACGATTT 3960
4434 Db GCTTGGGTTCAATGTTTACCGATGAAAAAGGTCAATAAAGGTGCTTTTGTGGAGACGATTT 4493
3961 QY CCGTTTGTATTTTCCAAAGGTTTGGATTTCCCTGACATTCAGTCAATGTGCTTAATCTCA 4020
4494 Db CCGTTTGTATTTTCCAAAGGTTTGGATTTCCCTGACATTCAGTCAATGTGCTTAATCTCA 4553
4021 QY TGTGGAATTTTGAAGCCAAACCTGTATAGAAAGGATTCGGTTACTTTTGTGGTAGATACA 4080
4554 Db TGTGGAATTTTGAAGCCAAACCTGTATAGAAAGGATTCGGTTACTTTTGTGGTAGATACA 4613
4081 QY TCATACACCATGATAGGAGGCAATAGTGTATATGATCTTTTGAAGTTCATCTCCAAAC 4140
4614 Db TCATACACCATGATAGGAGGCAATAGTGTATATGATCTTTTGAAGTTCATCTCCAAAC 4673
4141 QY TTGGGCAAAACATATCAAGGATTTAGTACATTTAGAGAGTTAAGGTTCTTTTGTGG 4200
4674 Db TTGGGCAAAACATATCAAGGATTTAGTACATTTAGAGAGTTAAGGTTCTTTTGTGG 4733
4201 QY ATGTGCTGTTGCTCGCTCGGAAACCTGTTAGGTTTCCGACGCTGAAACGACGATACA 4260
4734 Db ATGTGCTGTTGCTCGCTCGGAAACCTGTTAGGTTTCCGACGCTGAAACGACGATACA 4793
4261 QY AGGAGTTTCAAAAAACCGGATTTGATGTTGCTTTTAAATGCTTTTAAACAAAAATTTT 4320
4794 Db AGGAGTTTCAAAAAACCGGATTTGATGTTGCTTTTAAATGCTTTTAAACAAAAATTTT 4853
4321 QY TGTGCTGATAAATTTTATTTTATTTTGAAGCTTTGTTTTTAAATGCTTTTAAACAAAAATTTT 4380
4854 Db TGTGCTGATAAATTTTATTTTATTTTGAAGCTTTGTTTTTAAATGCTTTTAAACAAAAATTTT 4913
4381 QY GTCAAAATTTAGCGAGTTTCAATGATCTTTTGAACACAGGATGATCTTCGGGATTCATG 4440

TURPEN, THOMAS
 TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
 PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
 FROM PLANT SOURCES
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Howrey & Simon
 STREET: 1299 Pennsylvania Avenue N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/828,029
 FILING DATE: 20-Apr-2004
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/962,527
 FILING DATE: 24-Sep-2001
 APPLICATION NUMBER: 09/037,751
 FILING DATE: 10-march-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Halluin, Albert P
 REGISTRATION NUMBER: 25,277
 REFERENCE/DOCKET NUMBER: 00801.0140.999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-463-8109
 TELEFAX: 650-463-8400
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6395 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: Genomic RNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-10-828-029-1
 Query Match 40.9%; Score 2034.2; DB 19; Length 6395;
 Best Local Similarity 44.4%; Pred. No. 0; Mismatches 1793; Indels 21; Gaps 4;
 Matches 2214; Conservative 957;
 QY 6 AAGGTAATTCCTGAGTTTCAAGGGAGGCTTTTAAACAGGTATGACAGAGCTCCACGAA 65
 DB 537 AAAACAGUCCCAACUUCCAAAGGAAGCAUUGACAGAUACGACAGAAUUCUGAAGAC 596
 QY 66 GTCTGCTGCTTAAACTTTTTCAGGATGTCGAAATACATCCGCCAGAGATAGTGATGA 125
 DB 597 GUGUGUGUACAAUUAUCCAGACAAUCCGACAUCCAGCGGAGUAGCAUUCAGGACGA 656
 QY 126 AGATAGCTGCTTCTGACAGCTTTGTATGATTTCTGTGATGATGATGATGATGATG 185
 DB 657 GUGUAGUCCAUUGCGUACAGCAUUAUUGACAUUACACAGCCAGCCAGUAGUUGCGG 716
 QY 186 TTAATATCTAAGAAATATACATGATGATGATGATGATGATGATGATGATGATGAT 245
 DB 717 CUUUGAGGAAAUUGUACUAGUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 776
 QY 246 CTAGACAGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 305
 DB 777 CUUUGAGUACUAGUACUAGUACUAGUACUAGUACUAGUACUAGUACUAGUACUAG 836
 QY 306 GATGTTCTTTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 365
 DB 837 AAGUAGACCUUUCUUGUACUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 896
 QY 366 ATCTTGCAATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 425

DB 897 AUUCUUAAGUAGUGUGGCAAAACUUCUCCGGCCUUAUAGAGAGAGUUAUAGAAAG 956
 QY 426 GAAATTTTGTAGTCACTAGGTTTAAATTTTGTGTTTGTAAATTTTACCAAGTAGATCTAT 485
 DB 957 GAGUUAUAGUACACAGAGUUAUACUGGUUUUUAAGUUUUAUAGAAUAGUUAUUAU 1016
 QY 486 ATTCTGTACAAGAGTGTAGACAAGTGGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 545
 DB 1017 CUUUGUACAAAGUGUGGCCCAUAAAAGUGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1076
 QY 546 GAAGAGCGCTTTGCTTACAAGAAACCTTTGGCCATGTTCAACACTGAAGAGCAATCTTT 605
 DB 1077 GAAGACGCAUGGCAUUAACAAAGACUUCUUGCAUUGUAGCAAGCGAGAGAAUCCUCC 1136
 QY 606 AGAGACACGCTTTCGTTTAACTTTTGGTTCCCTTAAGATGAAGGACATGTGTAGTACCG 665
 DB 1137 GAGGAUUAUAGUACUAGUUAUACUGGUUUUCCCAAAUAGGGAUUAUGUACUAGUAC 1196
 QY 666 CTGTTTGGAGGTTCTATTACAGCAAAAGATGACAAGAGTGTAGTGTAGTGTAGTGTAG 725
 DB 1197 UUAUUGCAUUCUUGGAGACUAGUAGAGAGCGCGCAAGGAAGUUCUAGUGUCCAAG 1256
 QY 726 GACTTCTGTTTACACAGTCTTAACTATATATATATATATATATATATATATATATAT 785
 DB 1257 GAUUCUGUGUUAUACAGUGCUUAACCAUUCUAGCAUACACGCGCAAGAGCUCUUA 1316
 QY 786 CAGAAAGTATTATCTTTCTGAGTCTATAAGATCCGCTGTATATATATATATATATAT 845
 DB 1317 GCAAAUUGUUUCCUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1376
 QY 846 GCTAGTCTGAAATGGGATGTAGATAAAGCAATTTCTTCAACCTTTGTCAATGATCTTCT 905
 DB 1377 GCGAGGUCGAAUUGGAGUGGACAAUUCUUGUUAUACUUCUUGUACUAGUAGUUA 1436
 QY 906 TTGCGACACTAAGCTGCTGCTTCAAGACGATATAGTAAATGGGAAGTTTCGTGCTTG 965
 DB 1437 CUGCAUACUAAAGCUGUCCUUAAGGAUGACUUAUGUAGCAUUAUUGUAGUAGUAG 1496
 QY 966 GATAAGACCACTTCTGAATTTTGGGATGAGTGGGCAAAATTTTGTGAAACGTTTTC 1025
 DB 1497 UGCAAAACGUGUGGCGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1556
 QY 1026 CCCACTATCAAAAGAGAGATTGGTGAAGCAAAATTTCTGGATGTAAAGTGAATGCTCTG 1085
 DB 1557 CCCUCCGUGAAAGAGAGACUUCUUGAACAGAGAAUUAUACAGAGUGGCGAGCGCA 1616
 QY 1086 AAGATCAAGATCCAGATCTGTATGTATGTCATGGAAGACAGGTTCTGTAGTGAATAC 1145
 DB 1617 GAGAUACAGGUGGCGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1676
 QY 1146 AAGTCTGAGGATTTACCGCATCTAGATATCAAGAAAGACTTAGAAGAGCTGAGCAATG 1205
 DB 1677 GCUUUGUAGCAUUGCGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1736
 QY 1206 TACGAGCGCTTATCAAGATTTATCTTAAAGGTTGCTGATTAATTCGATATTCGGAAG 1265
 DB 1737 UACAAUACUUAUAGAGUUAUUGGUUAAGGAGUAGUAGUAGUAGUAGUAGUAGUAG 1796
 QY 1266 TTCAAGAGATGTGCAAGGCTTTAGATGTTAGTGTCTGTATGTGTGACAGCAGTATCG 1325
 DB 1797 UUUUCCAGUAGUGGCAUUCUUGGAAUUGGCCAACCCAAUAGCAGCGCAAGGUAUAG 1856
 QY 1326 GCATGCGCCGAGATAGAGCGGTTTAACTCTTACTTTTGTAAAGCAACCGAGAGAAAT 1385
 DB 1857 GCGGUACUAGAGUAGAGGCGGUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1916
 QY 1386 GTGGCTTAAGGCTCT-----TAAAGCAGCGGCTCTGAGGCGGCTGTATGTTGAACCG 1439
 DB 1917 GUUGCGCUAGCUUACAGGAUACAGGAAGAGGCUUACAGAGGUGCAUUGGUAGUAC 1976
 QY 1440 ACATCCGAAGAGGTGAACGTAATAATTTCTTATTTCTGCTGAGAAAGGAGATTCCT 1499

Db 1977 AGAGAAUGUAGAAACCGUCCAUAGAGGGUUGUAGUCCGACAGAGAGAGUUAUUAAGCU 2036
Qy 1500 TGTCCAGAAAGTCAATGTTTGACCAATGCCTAACTTAGAGACACGAGAGTGTGGATCCCTC 1559
Db 2037 GGUUCUGGAGAUCAUCGGAGUCGUCCUAUUAAGAACGAGGAGAGUAGUCUUUA 2096
Qy 1560 AACGATTTCCNATAGGCTTGGTGATGTGTGATTAACAAGCMAATGGCATCGTGTGTC 1619
Db 2097 GAGCAGUUUAUAGGCGGACAGUUCGUUAUUCGUUAAGCAGUAGCUCGUAUUGUG 2156
Qy 1620 TACACTGGCTCACTCAAGTTCAACAAATGAAGAACTATGTGACAGTTTGGCAGCTTCG 1679
Db 2157 UACACGGUCCGUAUUAAGUUCACAAUAGAAACUUUAUCGUAAGCCUGUAGCAUCA 2216
Qy 1680 TTGTCCGCCACTGATCAATCTATGCAAGTCACTAAAGGATGAAGTCGGGTATGATTC 1739
Db 2217 CUUUCUGCGGUGUGAUCUCGUAUUAAGUUCUAAAGUUAUAGUAGCCUU 2276
Qy 1740 GATTCCAGGAGAAAGTTGGTGGGATGTCACTTTGAAAMAAGTGGCTCCTCAAACT 1799
Db 2277 GAAACCGGUCAAAAGUUGGAGUCUUGAUGUUGAUCUAGGAAGUGGUUAUCAAACCA 2336
Qy 1800 GCGGCCAAAGTCAATCATGGGAGTTGTCTCGATTAACAAGGGGAAATGTTTACTGCA 1859
Db 2337 ACGCCAAGAGUAGUAGGUGGUGUUGUUGAAACCCACGGAGAGAUUAUAGUGGCG 2396
Qy 1860 CTTCTATCTTATGAAGGAGATAGAAATGGTGACTGAGAGCGACTGGAGGAGGTGGCTGTA 1919
Db 2397 CUUUGNAUUAUGAUGAGCAGGUGUGUGACUUGCGAUGAUUGGAGAGAGUAGUCUU 2456
Qy 1920 TCATCTGATCAATGGTATATCTGATATTTGCAAGCTCCAAATCTGAGGAAACAATG 1979
Db 2457 AGCUCUGAGUCUGUUGUUUAUUCGACAUUGCGGAAACUCAGAACUCUCGCGCAGUCUU 2516
Qy 1980 AGAGACGTGAACCCACGAACTTACTGCAAGATGTTGTTGGATGGGTCCTCGGT 2039
Db 2517 CGAAACGGAGAACCGCAUGCAGUAGCGCAAGGUGUUGUUGGAGCGGAGUUGCCGGC 2576
Qy 2040 TGTGAAAGTACAAAGGAGATTTTGAAGATTTGATCTTGATGAGGATTTGATCTTGTT 2099
Db 2577 UUGGAAACCAAGAAAUUUCUCCAGGUGUUAUUGAUGAAGAUUAUUAUUAUGA 2636
Qy 2100 CCGGAAACCAAGCTGCTGATGATCAGAGAGAGGCTAATTCATCTGGACTGATAGA 2159
Db 2637 CCUGGAGCAAGCCGCGGAAUUGAUGACAGACGUGCGAAUUCUCAGGGAUUAUUG 2696
Qy 2160 GCCAATGGAATGTGAGAACGTAGATTCATCTTAATGATCTTCTAATGATCTTCTA 2210
Db 2697 GCCAGAGGACACGUAUUAACCGUUAUUCUUGAUGAUGAUAUUGGAAAGACACA 2756
Qy 2211 CCGCGATCACAAGAGGCTTTTATTTGATGAAGGTTGATGCTGCACACCGTTGTGTT 2270
Db 2757 GCGUGAGUUAUAGAGGUUAUUAUUGAUGAAGGUGUUGUUGAUCUUGUUGUUGU 2816
Qy 2271 AACTTCTGTGCTTATCTCTGTTTGCACATCGATACATTTACGAGATACACAGCAG 2330
Db 2817 AAUUUUCUGUGGGAUGUUAUUGUGGAAUUGCAUUGUUGUUGCGGAGACACACGAG 2876
Qy 2331 ATTCTTTTCAATTAACAGATTCAGAAATTTCCGTTATCCCAACATTTTGAAGCTGCAA 2390
Db 2877 AUUCAUAUUAUAGAUUUCAGGAUUCUUGUUAUUCUUGGCGCCCAUUAUUGGAAUUGNA 2936
Qy 2391 GTGATGAAGTTGATGAGGAGGACCACTGAGATGCCAGGTGATGTGAATTTTTC 2450
Db 2937 GUUGACGAGGUGGAGACACGAGAAUUAUUCUUGUUGUUGCGGAGUUCACACAUUA 2996
Qy 2451 CTACATCGAAGTACGAAGGACGGTGACACCACTTCACTGTACACGATCGGTCTCA 2510
Db 2997 CUGAACAGGAUUAUAGGGGCUUUGAUGAGCAUUCUUGCGGUUAUUAAGUCUGUUGC 3056
Qy 2511 TCTGATGATAGGGGTAAGGGAGTACTAAACAGTGTTCACAACTTAAAGGAGAA 2570
Db 3057 CAGGAGUUGGCGGAGCCGCGUGAUCUAUCCGAUCUCAAACCCUUGUUGGCAAG 3116

Qy 2571 ATTGTAACTTTCACTCAGGCTGATTAATTTTGAAGAGGCTTATAAGATCTG 2630
Db 3117 AUCUGACUUUAACCAUUCGGAUUAAGAGCUCUUCUUAAGAGGUAUUCAGAUU 3176
Qy 2631 AACACGGTTTCATGATCCAGAGGAGAAACCTTTTGAAGATGTGCTGGTGGTCAGATTGACG 2690
Db 3177 CACACUGUGAUGAAGGCGAGCGAGACAUACUCUGAUGUUCACUAGUUGUUAUAC 3236
Qy 2691 GCAACTCCACTGATCTCTGATTTTCCAAAGTCTTCCCGCATGTTCTAGTCTCTGACTAGA 2750
Db 3237 CUUACACCAAGCUCUUAUGCAGGAGACAGCCCAUGUUAUUGGUGCUGAUUGCAAG 3296
Qy 2751 CACACAAAGACTTCAAAATTAACAAGTAGTGTGTAGTCTTGTAGTACAGATAATAGT 2810
Db 3297 CACACCUUGUGCGUCAAGUACUACACUGUUGUUAUGAUCUUAUUAUUAUUA 3356
Qy 2811 GATTGTCTTCTTTAAGCTCTTCTTTTAGAAATGTATATGTAGAACGAGGTAGTAGA 2870
Db 3357 GAUCUAGAGAAACUUAAGCUCGUACUUGUUAUUAAGUUAAGGUCUGAUCAGGAAACAA 3416
Qy 2871 TAGCAATTAACAGATGGATGAGTGTTCAAAGGTCAATAATCTTCTTGTGGCAACCTTAA 2930
Db 3417 UAGCAAUUAACAGAUAGCUGGUGUUCAAAGGUUCCAAUUCUUAUUGUGCAGGCCAAAG 3476
Qy 2931 TCAGGAGACTTTCCAGATCTACAGTCTTATACGATGTATGCTCTCCTCTGTAATAGTACT 2990
Db 3477 ACUGGUAUUAUUGAUGCAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3536
Qy 2991 ATACTTAAACAAGTATGATGCTGTTACCATGAGGTAGCTGATATAGTCTTAAATGTGAAG 3050
Db 3537 AUGAUAUAUUAUUGAUGCUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3596
Qy 3051 GATTGTGTTCTTGAATTTTCCAAAAGTATTTCCGATGCCAAAGAGGTGAACACCATGCTTA 3110
Db 3597 GAUUGCAUUAUGAUGAUGUUAUUGUGCGCCUUAAGAUCAUUAUUAUUAUUA 3656
Qy 3111 GAGCAGTGTTCGCTACCGCGCGGAAACCCGCAAGGGCTCAGGACTACTCGAAAATCTG 3170
Db 3657 AUACUUGUAGCAACCGCGGAGAAUUGCCGAGACUGGACUUAUUGGAAAUUA 3716
Qy 3171 GTTGCAATGATTAAGAAATTTCAACGACACAGACTGACGGGAGCGATTGACATTTGAG 3230
Db 3717 GUGCGAUGAUAUUAAGAAACUUUAACGACCCGAGUUGUUGGCAUUAUUAUUA 3776
Qy 3231 AGCACCGCATCTGTGTGTAGATAAGTATTTTGTATAGCTATTTTATTAAGAAAGAAAA 3290
Db 3777 AAUACUGCAUUCUUGUUGAUAUAUUAUUAUUAUUAUUAUUAUUAUUA 3836
Qy 3291 TACACAAAAATATTGCTGAGTGAACGAAAGATTCAATGATGAGATGTTGGAAGAAC 3350
Db 3837 AAACCAAAUAAAAUUGUUCUUGUUCAGUAGAGAGUCUCUUAUUAUUAUUA 3896
Qy 3351 AGGAAGAAGTACTATTGGACGACTTGGCTAACTACAAATTTTACAGATCTGCCGCCATC 3410
Db 3897 CAGAACGUAACAAUAGCCAGCUGCAGAUUAUUAUUAUUAUUAUUAUUAUUA 3956
Qy 3411 GATCAGTAAAGCAGACATGATCAAGGCTCAACCAAAACAGAAAAATTTGACCTTTCAATTGAG 3470
Db 3957 GAUCAGUACAGACAGAUUAUUAAGCAACCCCAACAAAGUUGGACACUUAUUAUUA 4016
Qy 3471 AATGAATACCTGCTCTGCAAAACAAATTTGCTACCTTTCGAGAGCAGATCAAGGTATTG 3530
Db 4017 ACGAGUACCCGCUUGCAGAGAUUGUGUUAUUAUUAUUAUUAUUAUUAUUA 4076
Qy 3531 GCGGTTTCTTCT--CAGAGCTTACAAGGTGCTGCTCGAGCATTTGATTTTAAAGAGTTT 3587
Db 4077 GGCCCGUUAUUAUAGUAGCUUAUUAUGCAUUAUUAUUAUUAUUAUUAUUA 4136
Qy 3588 CTTTTTCTTTACTAGAAAACTCCAGAAACAGATTCAGAAATTTTCTCGGATCTCGACTCG 3647
Db 4137 UUGUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4196


```
RESULT 6
US-10-338-592-2
; Sequence 2, Application US/10338592
; Publication No. US20030208792A1
; GENERAL INFORMATION:
; APPLICANT: Fitch, John H.
; APPLICANT: Beachy, Roger N.
; TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS TO
; TITLE OF INVENTION: OVERPRODUCE PEPTIDES AND PROTEINS
; FILE REFERENCE: TSRI 312.1C1
; CURRENT APPLICATION NUMBER: US/10/338,592
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 09/401,415
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 08/687,559
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: PCT/US95/01467
; PRIOR FILING DATE: 1995-02-03
; PRIOR APPLICATION NUMBER: US 08/192,477
; PRIOR FILING DATE: 1994-02-03
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 6395
; TYPE: DNA
; ORGANISM: Tobacco mosaic virus
US-10-338-592-2

Query Match 40.8%; Score 2031; DB 17; Length 6395;
Best Local Similarity 63.6%; Pred. No. 0;
Matches 3169; Conservative 0; Mismatches 1795; Indels 21; Gaps 4;

QY 6 AAGTAAATCTCGAGTTTCAAGGGAGGCTTTTAAACAGGTATGCAGAACTCCCAAGAA 65
DB 537 AAAACAGTCCCAACTTCCAAAGGAAGCATTTGACAGATACGCAGAAATTCCTGAAGAC 596
QY 66 GTCTGCTGCTTAAACTTTTCAGGATTTGCGAATACATCCGCGACAGAAATAGTGTAGA 125
DB 597 GTGTCTGTCACAAATCTTCCAGCAATGCGGACATCAGCGGATGCGCAATCAGGCAGA 656
QY 126 AGATAGCTGTGCTCTGCACAGTTTGTATGATATTCCTGTGATGAGTTTGGAGTGGC 185
DB 657 GTGTATGCCATTTGGCTACACAGCATATATGACATACACGCGATGAGTTTGGGGGGCA 716
QY 186 TTAATATCTAAGAAATATACATGATGTTATGACAGTTTCAATTTTGGCAGAGCAATTA 245
DB 717 CTCTTGAGGAAATATGTCATACGTGCTATGCGGCTTTCACCTTCTCTGAGAACCTGCTT 776
QY 246 CTAGACGACGAGGTTACGCTTAAATGAATAGGCGCAACTTTTCAAAAGAGAGGTGAT 305
DB 777 CTTGAAGATCTACGCTCAATTTGGAGCAATCAACGCGTGTGTTTTCGCGCGATGAGAC 836
QY 306 GATGTTTCTTTTCTTTGCTGATGAAGTACTTTTAAATTTATAGTCAATAAACAATAAT 365
DB 837 AAGTTGACCTTTTCTTTTGCATCAGAGTACTTCTTAAATTTATGTCATAGTTTCTAAT 896
QY 366 ATCTGCAATATGATGATTAATCTTATCTTCTGCTTCTAGTGAATAGTTTACTTTAAG 425
DB 897 ATCTTTAAGTATGTTGCAAACTTACTTCCCGGCTCTAATAGAGAGGTTTACATGAAG 956
QY 426 GAATTTTGTACTAGGTTTATCTTGTGTTTGTAAATTTTAAATTTTAAAGTAGATCTAT 485
DB 957 GAGTTTGTAGTCCAGAGTTAATACCTGTTTGTAAAGTTTCTAGATAGATATCTTTT 1016
QY 486 ATTCTGTACAAGAGTGTAGACAAGTAGGTTGATAGTATGATGATGATGATGATGATG 545
DB 1017 CTTTGTACAAGAGTGTGGCCCTTAAAGTGTAGATGATGAGCAGTTTATATCTGCAATG 1076
QY 546 GAAGAGCCCTTTGCTTACAAGAAAACTTGGGCCATGTTTCAACCTGAAGAGCAATCTTT 605
DB 1077 GAAGAGCCATGCGATTAACAAAAAGACTCTTGTGCAATGTGCAACAGCAGAGAACTCT 1136
```

```
QY 606 AGAGACACGGCTTCGGTTAACTTTTGGTTCCTTAAGATGAAGGACATGCTGTAGTACCG 665
DB 1137 GAGGATTCATCATCAGTCAATTTACTGGTTTCCAAAATGAGGATATGCTCATCGTACCA 1196
QY 666 CTGTTTGGGGTTCTATTACCAGCAAAAGATGACAAGAGTGAGGTCAATCTGTTAATCGT 725
DB 1197 TTTATTCGACATTTCTTTGGAGACTAGTAGAGGACCGCAAGAAAGTCTTAGTGTCCAAG 1256
QY 726 GACTTCGTTTACACAGTCTTAATCATATCAGAAATATCAAGCCAAAGCGTTTAACTTAC 785
DB 1257 GATTTCTGTTTACAGTCTTAACCAATTCGAACATACCAAGCGCAAGCTCTTACATAC 1316
QY 786 CAGAACGATTAATCTTTTGGGAGTCTATAAGATCCCGGTGATTAATCAATGGTGTACT 845
DB 1317 GCAAAATGTTTGTCTCTTTGCGAATCGATTCGATCGAGGGTAAATCATTAACGGTGTGAC 1376
QY 846 GCTAGTCTGAATGGATGTAGATAAAGCAATTTCTCAACCTTGTCAATGACTTTCTTTC 905
DB 1377 GCGAGTCCGAATGGGATGTGACAAATCTTTGTACAACTCTTGTCCATGACGTTTAC 1436
QY 906 TTGCAGACTAAGCTGGCTCGCTTCAAGACGATATAGTAATGGGAAAGTTTCGGTCTTG 965
DB 1437 CTGCATCTAAGCTTGGCTTCTTAAGGATGACTTACTGATTAGCAAGTTTAGTCTCGGT 1496
QY 966 GATAAGACACTTCTGAACTTAATTTGGGATGAGGTGGGCAAAATTTTGGAAACGTTTTC 1025
DB 1497 TCGAAAAACGGTGTGCGCAGCATGTGCGGATGAGATTTTCGCTGCGCGTTTGGGAAACG 1556
QY 1026 CCCACTATCAAGAGAGATTTGGTGAGCAGGAAATTTCTGGATGTAGTCAGAAATCTCTG 1085
DB 1557 CCCCTCCGTAAGAGAGGCTTGTGAACAGGAACTTTTACAGAGTGCAGCGACGCAATTA 1616
QY 1086 AAGATCAAGATCCAGATCTGTATGTCTCATGCGAAAGACAGGTTCTGTAGTCAATACAC 1145
DB 1617 GAGATCAGGTCCTGATCTATATGTGACTTCCACGACAGATTAGTACTGAGTACAAG 1676
QY 1146 AAGTCTGAGGAGTTACCGCATCTAGATATCAAGAGAGACTTAGAAGAGCTGAGCAATG 1205
DB 1677 GCCTCTGTGACATGCTCGCTTGACATTTAGGAGAGATGGAAGAAACGGAAGTGTG 1736
QY 1206 TAGCAGCGTTATCAGAAATATCTATCTTTAAGGTGCTGTAAATTTTCCATATCGCGAAG 1265
DB 1737 TACAATGCACTTTTCAAGATTTATCGGTGTTAAGGGAGTCTGACAAATTCGATGTTGAT 1796
QY 1266 TTTCAAGACATGTGCAAGGCTTTTAGATGTTAGTCTCTGTATGTGCGCAGCAGGTAAT 1325
DB 1797 TTTTCCAGATGTGCCAATCTTTGAGAGTTGACCAATGACGCGCAGGAGGTTATAGTC 1856
QY 1326 GCAGTGGCGGAGAAATAGAGCGGTTTAACTCTTTAATTTTGTGTAAGCCACCGAGGAGAT 1385
DB 1857 GCGGTCTAGCAATGAGAGCGGCTCTGACTCTCACAATTTGAACGACTTACTGAGGCGAAT 1916
QY 1386 GTGGCTAAGCTCT-----TAAAGCAGCGGCTCTGAGCGCTGTGATGCTCTTGAACCG 1439
DB 1917 GTTGGCTAGCTTTACAGGATCAAGAGAGGCTTCAAGAGGCTCTTGGTAGTTACTCTCA 1976
QY 1440 ACATCCGAAGAGGTGAACGTAATAATTTTCTATTGCTGAGAAAGGAGATTTGCTGTG 1499
DB 1977 AGAAGAGTTGAAGAACCGTCCATGAAGGTTTCAAGCGCCAGGAGAGTTTACAATTAGCT 2036
QY 1500 TGTGCAAGAAAGTATGTTTGAAGATGCTAACTTAGAGCACAGAGGTTGGAGTCCCTC 1559
DB 2037 GGTCTTGTGGAGATCATCCGGAGTCTCTTCTTCTTAAAGAACGAGAGATAGAGTCTTTA 2096
QY 1560 AAGATTTCCATAGGCTTGGCTGAGTGTGATTTACAAGCAATGCGATCGGTTGTC 1619
DB 2097 GAGCAGTTTTCATATGCAACGCGCAGATTCGTTAAATTCGTAAGCAGATGAGTCTGATG 2156
QY 1620 TACACTGGCTCACTCAAGTTTCAACAAATGAAGAACTATGTGACAGTTTGGCAGGCTTCG 1679
DB 2157 TACAGGGTCCGATTAAGTTTCAAGAAATGAAGAACTTTTATCGATAGCTGTTAGCATCA 2216
QY 1680 TTGTCCGCCACTGTATCAAAATCTATGCAAGTCACTAAAGGATGAAGTCCGGTATGATCT 1739
```

Db	2217	CTATCTCTCGCGTGCAGATCTCGTCAAGATCCTCAAGATACAGCTGCTATTGACCTT	2276
Qy	1740	GATTCCAGGAGAAAGTTGGTGTGTTGGGATGTCACTTTGAAAAAGTGGCTCTCCAACCT	1799
Db	2277	GAATCCCGTCAAAAGTTGGAGCTTGGATGTTGCATCTAGGAAGTGGTTAATCAAAACCA	2336
Qy	1800	CGGCCCCAAGGTCATTCATGGGAGTTGTCTCTGATTTACAAGGGGAAAAATGTTTACTGCA	1859
Db	2337	ACGGCCAAGAGTCATGATGGGTGTTGTTGAAACCCACCGAGGAAGTATCATGTGGCG	2396
Qy	1860	CTTCTATCTTATGAAGAGATAGAAATGGTGACTGTGAGAGCACTGGAGGAGGGTGGCTGTA	1919
Db	2397	CTTTTGGAAATATGATGACGAGGGTGTGGTGAACATGCGATGATTGGAGAGAGTAGCTGTC	2456
Qy	1920	TCATCTCATACAATGGTATATCTGATATTGCGAAAGCTCCAAAATCTGAGGAAAACAATG	1979
Db	2457	AGTCTCAGTCTGTGTTTATTCGACATGGCGAACTCAGAACTCTGCGCAGACTGCTT	2516
Qy	1980	AGACCGGTGAACCCCAAGAACCTACTCTGCAAGATGGTACTTGTGGATGGGGTGCCTGGT	2039
Db	2517	CGAAAACGAGNACGCAATGTCAGTAGCGCAAGGTGTCTTGTGACGGAGTTCGGGC	2576
Qy	2040	TGTGGAAGTACAAGGAGATTTTGAAGATTTTGATCTTGATGAGGATTTGATCTTGGTT	2099
Db	2577	TGTGGGAAAAACCAAGAAATCTTTCCAGGGTTAAATTTTGATGAAGATCTAAATTTAGTA	2636
Qy	2100	CCTGGAAAAACAGCTGCTGTATGATCAGAAAGAGGGCTAAATCATCTGACACTGATAAGA	2159
Db	2637	CCTGGGAAGCAAGCCGGGAAAAATGATCAGAAAGCTGCGAAATTTCTCAGGGAATATTGTG	2696
Qy	2160	GCCAAATGACAAATGTGAGAAACGGTAGATTCACTTCTAATGCAT-----CCAAAA	2210
Db	2697	GCCACGAGGACACGTTAAAAACGTTGATCTTTTATGATGAATTTTGGGAAAAACACA	2756
Qy	2211	CCGCGATCACACAAGAGGCTTTTATTGATGAAGGGTTGATGTGCAACAACGGTTGTGTT	2270
Db	2757	CGCTGTCAGTTCAGAGGTTATTCAITTGATGAAGGGTTGATGTGTCATCTGGTTGTGTT	2816
Qy	2271	AACCTCTGGTCTTATCTCTGGTTGGACATCGCATACATTTACGGAGATACACAGCAG	2330
Db	2817	AAITTTCTTGTGGCGATGTCAATGTGCGAAATTGCAATGTTTACGGAGACACACAGCAG	2876
Qy	2331	ATTCCTTTCTAATAACAGAGTTTCAGAAATTCCTCGTATCCCAAAACATTTTGAGAAGCTGCAA	2390
Db	2877	ATTCATACATACAGTTCAGGATTCGCGTACCCGCTACCCGCCCATTTTGGCCAAATGGAA	2936
Qy	2391	GTGGATGAAGTTTGATGTAGAGGACCAACTGTAGATGCCCAGGTGATGTAATTTTTTC	2450
Db	2937	GTTACGAGGTGGAGACACGCAGAACTACTCTCCGTTGTCCAGCCGATGTCAACATTAT	2996
Qy	2451	CTACAATCGAAGTACGAGGAGCGGTGACAAACCACTTCAACTGTGTACAAACGATCGGTCTCA	2510
Db	2997	CTGAACAGGAGATATAGGGCTTTGTTCATGAGCACTTCTTCGGTTAAAAAGTCTGTTTCG	3056
Qy	2511	TCTCAGATGTATGCGGTGAAGGAGTAGTAAACAGTGTTCCTCAAAACCACTTAAAGGGAAA	2570
Db	3057	CAGAGATGTGCGCGGAGCGCCGTGATCAATCCGATCTCAAAAACCTTGCATGGCAG	3116
Qy	2571	ATTGTAACTTTTACTCAGGCTGTATAAATTTGAGTTAGGAGAGAGGCTATAAGAAATGTG	2630
Db	3117	ATCCTGACTTTTACCCTAATCGGATAAAGAAAGCTCTGCTTTTCAAGAGGGTATTTCAGATGTT	3176
Qy	2631	AACACCGTTCATGAGATCCGAGGAAACCTTTGAAGATGTGTGCTGGTTCAGATTGACG	2690
Db	3177	CACACTGTGCATGAAGTGCAGAGGAGACATCTCTCATGTTTTCACCTAGTTAGGTAAACC	3236
Qy	2691	GCAACTCCACTGACTCTGATTTCCAAAGTCTTCCCGCGATGTTCTAGTCTGCTCTGACTAGA	2750
Db	3237	CCTACACGAGTCTCCATCAATTCGACGAGACAGCCCAACATGTTTTGGTTCGCAATGTCAAGG	3296
Qy	2751	CACACAAAGAGCTTCAAATATTAACCGGTAGTGTAGATCTTTTGTAGTACAGATAATTTAGT	2810

3297	Qy	3297	Db	CACACCTGTTCCGCTCAAGTACTACACTGTTGTTATGATGCTCTTTAGTTAGTATCATTTAGA	3355
2811	Qy	2811	Qy	GATTTTGCTCTTTTAAAGCTCCTTTCCCTTTTAAAGAAATGTATATGTTAGAAAGCAGGTAGTAGA	2870
3357	Db	3357	Db		3416
2871	Qy	2871	Qy	GATCTAGAGAAACTTAGCTCGTACTTGTGTAGATATGATAAAGGTCGATGCAGGAACACAA	2930
3417	Db	3417	Db	TAGCAATTAACAGATGAGTGTCTTCAAAAGGTCATAATCTCTTTGTGGCAACACCTTAAA	3476
2931	Qy	2931	Qy	TAGCAATTAACAGATGAGTGTCTTCAAAAGGTTTCAAAATCTTTTGTGTCAGCGCCCAAG	2990
3477	Db	3477	Db	TCAGGAGACTTTCCAGATCTACAGTGTCTATTAACGATGTATGCTCTCCCTGCTGTAAATGTPACT	3536
2991	Qy	2991	Qy	ACTGGTGATATTTCTGATATGCAATTTTACTATGATAAGTGTCTCCAGGCAACAGACCC	3050
3537	Db	3537	Db	ATACTTAAACAAGTATGATGCTGTTTACCATGAGGTTACGTGATATAATAGTCTTTAATGTGAAG	3596
3051	Qy	3051	Qy	ATGATGATTAATTTTGTGCTGTTTACCAAGAGGTTGACTGACATTTTCAATGTAATGTCAAA	3110
3597	Db	3597	Db	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3656
3111	Qy	3111	Qy	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3170
3657	Db	3657	Db	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3716
3171	Qy	3171	Qy	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3230
3717	Db	3717	Db	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3776
3231	Qy	3231	Qy	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3290
3777	Db	3777	Db	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3836
3291	Qy	3291	Qy	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3350
3837	Db	3837	Db	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3896
3351	Qy	3351	Qy	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3410
3897	Db	3897	Db	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3956
3411	Qy	3411	Qy	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3470
3957	Db	3957	Db	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	4016
3471	Qy	3471	Qy	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3530
4017	Db	4017	Db	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	4076
3531	Qy	3531	Qy	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3587
4077	Db	4077	Db	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	4136
3588	Qy	3588	Qy	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3647
4137	Db	4137	Db	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	4196
3648	Qy	3648	Qy	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3707
4197	Db	4197	Db	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	4256
3708	Qy	3708	Qy	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3767
4257	Db	4257	Db	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	4316
3768	Qy	3768	Qy	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3827
4317	Db	4317	Db	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	4376
3828	Qy	3828	Qy	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	3887
4377	Db	4377	Db	GATTTGATATTTGATATATGTTCTAAAGTCTGTTGCTCGCTAAAGGATCAAAATCAAAACCACTA	4436

3888 ATATAGCAGCTTGGTGGTTCAATGTTACCGATGGAAGGTCATAAAGGTCGTTT 3947
 Db |||||
 4437 ATCATGCTGATGTTGGCTCGATCTCGATGGAGAAATATCAAGAGCGCTTT 4496
 Qy |||||
 3948 TGTGAGACGATTCGGTGTATTTTCCAAAGGTTTGGATTTCCCTGACATTCAGTCA 4007
 Db |||||
 4497 TCGGTTGACATAGTCTGCTGATTTTCCAAAGGTTTGGATTTCCGATGTCACAC 4556
 Qy |||||
 4008 TGTGCTAATCTCATGTTGGAATTTTGGAGGCTTGTATAGAAAGGTTACGTTACTTT 4067
 Db |||||
 4557 TCCGGAATCTTATGTTGGAATTTTGAAGCAAACTGTTTAAAGAAACAGTATGGATCTTT 4616
 Qy |||||
 4068 TGTGTTAGATACATCATACCATATGATGAGGAGCAATAGTGTATATGATCTCTTTGAAG 4127
 Db |||||
 4617 TCGGAGATATGTAATACATACGACAGAGATGATGTTGATTAACATCCCTTAAG 4676
 Qy |||||
 4128 TTGATCTCAAACTTTGGGCAAAACATATCAAGGATTTATGATCATTTAGAAAGTTAAGG 4187
 Db |||||
 4677 TTGATCTCGAACTTTGGTCTAAACATCAAGGATTTGGAACTTTGGAGGATTCAGA 4736
 Qy |||||
 4188 GTGCTTTTGGATGTTGCTGCTCGGAACTGCTTAGGCTTTCCGAGCTG 4247
 Db |||||
 4737 AGGTCTCTTTGATGTTCTGTTCTGTTTCTGTTT--GAACAATTTGTCGATTAACACAGTTG 4793
 Qy |||||
 4248 AACGAGCTATCAAGGAGGTTTCATAAAACCGGATTTGATGTTTCTGTTTCTTTAATCTG 4307
 Db |||||
 4794 GAGGAGCTGTATGGAGGTTTCATAAGACCGCCCTCCAGTTCGTTTGTATATAAAGT 4853
 Qy |||||
 4308 GTTAAACAAATTTTGTGTGATAAATTTTATTTAGAACTTTGTTTAAATGCTGTTAG 4367
 Db |||||
 4854 CTGGTGAATTTTGTCTGATAAGTTCTTTTATGAAAGTTTGTATATAGTCTCTAGT 4913
 Qy |||||
 4368 TCTCAGAGATCTGTCAAAATTTAGCGAGTTTCAATGATCTTTTCAAAACAGATGAGATCT 4427
 Db |||||
 4914 TGTAAAGGAAAGTGAATATCAATGAGTTTATCGACCTGACAAAAATGGAGAATCTT 4973
 Qy |||||
 4428 TCCGGATTCATGACTAAGTCAAGAGTGTGTAATATCGACTGTCGACAAAGATTTATGGC 4487
 Db |||||
 4974 ACCGTGATGTTTACCCCTGTAAAGAGTGTATGTTTCAAGTTGATATAATATGTT 5033
 Qy |||||
 4488 TGTAAAGATGATGATGTTCTTTCTGATGTAGATTTTACTTAAAGGTTGTTAAGTTAGTAA 4547
 Db |||||
 5034 TCATGAGATGATGATGTTCTGATGAGTGAACCTTTTAAAGGATTTAAGCTTATGATAG 5093
 Qy |||||
 4548 AGGTTATGTTGCTTATGATGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 4607
 Db |||||
 5094 TGGATACGTTCTGTTTATGCGGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5153
 Qy |||||
 4608 CCGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 4667
 Db |||||
 5154 CAGAGAGGTTGTTGAGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5213
 Qy |||||
 4668 GCTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 4727
 Db |||||
 5214 TCTCGATCTTACTACACAGCAGCTGCAAGAAAGATTTTCAAGTTCGTTTCCCAA 5273
 Qy |||||
 4728 TTATTCATTAACATCCGAGATCTGAGAGCAACCGTGGCAAGTGTAGTGAATATCAA 4787
 Db |||||
 5274 TTATGCTATTAACACCCAGGACGATGAAACCGTCTGGCAAGTTTATGTTAATATAG 5333
 Qy |||||
 4788 AGGAGTGGCTATGGAAGAGATCTGCTCTTTATCTTTGAGTGTGTTTCAATTTGTTGTT 4847
 Db |||||
 5334 AAATGGAAGATGTACGCGGTTTCTGTCGCTTTCTCTGAGGTTTGTGTCGGTGTAT 5393
 Qy |||||
 4848 AGTACATAAAATAATGTAAGAAAGGTTTGGAGAACGTTATTTGAGTGTGACAGACGG 4907
 Db |||||
 5394 TGTTTATAGAAATATAATAATTTAGTTTGGAGAGAGATTTACAACTGAGAGACGG 5453
 Qy |||||
 4908 CTCGCCAATTTGAATCTCACTGAAAGGTTTGTGAGGAGTTTCTGAGTGAAGTCAATGGC 4967
 Db |||||
 5454 AGGGCCCATGGAATTTACAGAGAGGTCGTTGATGATGTTTATGAGTTCATGGAAGATGTCCTATGTC 5513

Qy 4968 TGTGA 4972
 Db 5514 GATCA 5518

RESULT 7
 US-09-962-527-3
 ; Sequence 3, Application US/09962527
 ; Publication No. US20030049813A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GARGER, STEPHEN
 ; HOLTZ, R. BARRY
 ; McCULLOCH, MICHAEL
 ; TURPEN, THOMAS
 ; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
 ; PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
 ; FROM PLANT SOURCES
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howrey & Simon
 ; STREET: 1299 Pennsylvania Avenue N.W.
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/962,527
 ; FILING DATE: 24-Sep-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/037,751
 ; FILING DATE: 10-march-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Halluin, Albert P
 ; REGISTRATION NUMBER: 25,277
 ; REFERENCE/DOCKET NUMBER: 00801.0140.999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-463-8109
 ; TELEFAX: 650-463-8400
 ; TELEX: <Unknown>
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6425 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: Genomic RNA
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 ; US-09-962-527-3

Query Match 40.8%; Score 2031; DB 10; Length 6425;
 Best Local Similarity 44.4%; Pred. No. 0;
 Matches 2212; Conservative 957; Mismatches 1795; Indels 21; Gaps 4;

Qy 6 AAGGTAATTCCTGAGTTTCAAAGGAGGCTTTTAAAGGATGTCAGAGTTCACAGAA 65
 Db |||||
 537 AAAACAGUCCCCAACUCCAAAGGAAGCAUUGACAGAUACGAGAAAUUCCUGAGAC 596
 Qy 66 GTCTGCTGCTCTAAACATTTTCAGGATTTGCGAATATCCGCCAGAGATAGTGGPAGA 125
 Db |||||
 597 GCUUCUGUCACAAUUCUUCGAGCAUUGCCGAGCAUUGCCGAGCAUUGCCGAGCA 656
 Qy 126 AGATACGCTGTTCTCTGACAGTTCGATGATGATTTCTGTCATGAGTTTGGAGTGGC 185
 Db |||||
 657 GUGUAGUCCAUUGCGCUACACAGCAUUAUGACAUACAGCCGAGCAUUGUUGCGGCGCA 716
 Qy 186 TTAATATCTAAGAATATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 245
 Db |||||

Db 717 CUCUUGAGGAAAAUUGUCCAUACGUGCUAUUGCCGCUUUUCCAUUCUCUGAGAAACCUUCUU 776
Qy 246 CTAGACAGACGGAGGTACGCTTTAAATGAATAGCGCGCAACTTTTCAAAGAGAGAGGTGAT 305
Db 777 CUUGAAGAUCAUACGUAUUGGACGAUAUCAAACGCGUGUUUUCGCGGAGGAGAC 836
Qy 306 GATGTTTTCTTTTCTTTGCTGATGAAGAGTACTTTTAAATTAATAGTCAATAATACAAAAT 365
Db 837 AAGUGAACCUUUUUUUUGCAUCAGAGAGAGUCUUAUAUUGUCAUAGUUAUUCUUAU 896
Qy 366 ATCTTGCAATATGATGATTAATCTTACTTCTCTGCTTCTAGTAGAATAGTTACTTTAAAG 425
Db 897 AUUCUUAAGUUGUGGCAAAACUUAUCUCCGCGCCUCUAUAGAGAGGUGUUUACUGAG 956
Qy 426 GAATTTTTAGTCACTAGGCTTAATACTTGTGTTTTGTTGTTAAATTTACCAAAGTAGATACCTAT 485
Db 957 GAGUUUUAGUCACGAGUUUAUACCGUGUUUUGAAGUUUUCUAGAAUAGAUACUUU 1016
Qy 486 ATTCTGTACAGAGTGTAGACAAAGTAGGGTGTGATAGTCAATGATTTCTATAGGGCGATG 545
Db 1017 CUUUGUACAAAGGUGUGGCCAUAAAAGUGUGAUGAUGAGCGAGCUUUUUAUCUGCAAUG 1076
Qy 546 GAGACGCCCTTGTCTTACAGAAACCTTGGCCATGTTCAACACTGAAAGAGCAATCTTT 605
Db 1077 GAAGACGAGGCAUUAUAAAAGACUCUUGCAUUGGCAACGCGAGAGAUCCUUCUU 1136
Qy 606 AGAGACACGGCTTCGGTTAACTTTTGGTTCCCTAAGATGAAGGACATGGTGATAGTACCG 665
Db 1137 GAGGAUUCAUCAUCAGUCAAUUAUCUGGUUUCCCAAAUAGAGGGAUUGGUCAUCGUACCA 1196
Qy 666 CTGTTTGAAGGTTCTATTACAGCAAAAAGATGACAGGAGTGAAGTCAATGTTAATCGT 725
Db 1197 UUAUUGACAUUUUUUGGAGACUAGUUAAGAGGACGCGCAAGGAAGUCUUGUCCUAAAG 1256
Qy 726 GACTTCGTTTACAGTGTCTTAATCATATCAGACATATCAAGCAAAAGCGTTAACTTAC 785
Db 1257 GAUUUCGUGUUUACAGUGCUUUAACCAUUCGAACAUACCGGCGAAAGCUCUUAUAC 1316
Qy 786 CAGAACGTATPATCTTTCTGAGGCTTATAAGATCCGCGGTGATPAATCAATGGTGTACT 845
Db 1317 GCAAAUGUUUUGUCCUUGCAUUGCAUUGAGGAGGGAUUAUCAUUAAGCGGUGACA 1376
Qy 846 GCTAGGCTGAATGGGATGATAGTAAGCAATCTTCAACCCTTGTCAATGACTTTCTTC 905
Db 1377 GCGAGGUCGGAAGGAGUGGACANAUCUUUGUUAUCAAUCUUGCCUUGCAUGUUUAC 1436
Qy 906 TTGCAGACTAAGCTGGCTGCGCTTCAAGACATATAGTAATGGGAAAGTTTCGGTGTG 965
Db 1437 CUGCAUACUAAAGCUUGCGUUCUUAAGGAUGACUUAUGAUUACGAUUUUAUGUCUGGU 1496
Qy 966 GATAAGACCACTTCTGAACTTATTTGGGATGAGGTGGGCAAAATTTTGGAAACGTTTTC 1025
Db 1497 UCGAAACCGGUGGCCAGCAUGUGGGAUGAGAUUUCGUGCGUUUUGGGAACGCAUUU 1556
Qy 1026 CCCATATCAAGAGAGATTTGGTGAAGGAAATTTCTGGATGTAAGTGAATGCTCTG 1085
Db 1557 CCCUCCUGGAAGAGAGGCGUCUUGAACACAGGAAACUUAUCAGUGGCGGCGAGCGCAUUA 1616
Qy 1086 AAGATCAAGATCCAGATCTGTATGTACATGGAAGAGACAGGTTCTGATGTAATACACC 1145
Db 1617 GAGAUACGGGUGGUGAUCUUAUUGUACCUUCCACGACAGAUUAGUGACUGAGUACAG 1676
Qy 1146 AAGTCTGAGGAGTTACCGCATCTAGATATCAAGAGGACTTTAAGAGAGCTGAGCAAAATG 1205
Db 1677 GCCUCUGGACAUCCGCUUGACAUUAGGAAGAAGUAGGAAGAAACGGAAGUAG 1736
Qy 1206 TACGACCGTTATCAGATATCTATCCTTAAGGGTCTGTATATTTTCGATATCGCGAG 1265
Db 1737 UACAAGCAUUCUUGAGUUUACGGUGUUUAGGGAGUCUCAGAAUUCGAGUUGUUGAU 1796
Qy 1266 TTCAAAGACATGTGCAAGGCTTTAGATGTTAGTCTCTGATGTGGCAGCAGCAAGTAACTGTT 1325
Db 1797 UUUUCCAGAUUGUCCAAUUCUUUGGAAGUUGACCCAAUAGACGGCAGCGAAGGUUAUAGUC 1856

Qy 1326 GCAGTGGCCGAGAAATAGAACGGCTTTAACTCTTACTTTTGTATTAAGCAACCGAGGAGAAAT 1385
Db 1857 GCGUUAUGAACCAUAGAGCGGUCUGACUCUCACAUUUGAAACGACCUACUGAGCGGAU 1916
Qy 1386 GTGGCTAAAGCTCT-----TAAAGCACGGCTCTGAGSCCGTGTGTATGTCTTGAACCG 1439
Db 1917 GUUGCGUAGCUUUAUAGGAUCAAGAGAGGCUUACAGAGGUCUUGUAGUUGUUAUCCUCA 1976
Qy 1440 ACATCCGAGAGGCTGAACGCTAAATAAATTTTCTATTGCTGAGAAAGGGAGATTGCCCTGTG 1499
Db 1977 AGAGAUGUAGAAGAACCGUCCUAGNAGGUGUCCUGAGGCCAGAGAGAGUUUAUAAUAGCU 2036
Qy 1500 TGTGCGAAGAGTCAATGTTGACGAATGCTAATTAGAGACCAGAGAGTTGGAGTCCCTC 1559
Db 2037 GGUUUGUGGAGAUCAUCGAGUGUGUCCUAUUUCAAAGAACGAGGAGAUAGAGUCUUUA 2096
Qy 1560 AACGATTTCCATAAGCTTCCGTGGATAGTGTATTACAAAGCAAAATGGCATCGTGTGTC 1619
Db 2097 GAGAGUUUCAUUGGCAACGCGCAGAUUCGUUAUUCGUAAAGCAGAGUAGCUCGAUUGUG 2156
Qy 1620 TACACTGGCTCACTCAAAGTTCAACAAATGAAGAACTATGTGGACAGTTTGGCAGCTTCG 1679
Db 2157 UACACGGUCCGAUUAAGUUCAGCAAAUGAAAAACUUUAUCCGAUAGSCCUGGUAGCAUCA 2216
Qy 1680 TTGTCGCGCATCTGATCAATCTATGCAAGTCACTAAAGGATGAAGTGGGTATGATCT 1739
Db 2217 CUAUUGUGUGGUGUGAUCUCGCAAGAUCCUCAAAGAUACAGCUGCUUAUUGACUU 2276
Qy 1740 GATTCCAGGAGAGAAAGTTGGTGTTCGGATGTCACTTTTGAAGAGTGGCTCTCAAACT 1799
Db 2277 GAAACCGUCAAAGUUUGAGUGUGGUGUUGCAUUCUAGGAAGUGUUAUCAAACCA 2336
Qy 1800 GCGGCCAAAGGTCATTCATGGGGAGTTGTCCTGGATTACAAGGGGAAAAATTTTACTGCA 1859
Db 2337 ACGGCCAAGAGUCAUGCAUGGGGUGUUGUUGAAAAACCCACCGAGGAAGUAUCAUGUGCG 2396
Qy 1860 CTTCTATCTTATGAAGAGATAGATGGTGACTGAGAGCGACTGGAGGAGGGTGGCTGTA 1919
Db 2397 CUUUGGAUUAUGAGACGAGGUGUGUGACAUGCAUUGGAUUGGGAAGAGUAGUGUC 2456
Qy 1920 TCATCTGATACAAATGGTATATCTGTATTTGCAAGCTCCAAATCTGAGGAAAAACAATG 1979
Db 2457 AGCUCUGAGUCUGUUUUUAUCCGACUGSCGAACUCAGACUCUCGCGCAGACUCUU 2516
Qy 1980 AGAGACGGTGAACCCCAACCTACTCTCAAGAGATGCTTGTGATGGGTGGCTGGT 2039
Db 2517 CGAAACGGAGAACCGCAUGUCAGUAGCGCAAAAGGUUUCUUGGACGCGAGUUCGCGC 2576
Qy 2040 TGTGGAAGTACAAAGAGATTTTGAAGATTTTGAATCTTGTGATGAGGATTTGATCTTGGTT 2099
Db 2577 UGUGGGAACCAAGAAAUUUUUUCCAGGGUUUAUUUGAUGAAGAUUUUUUUAAGUA 2636
Qy 2100 CTTGGAACCAAGCTGCTGCTATGATCAGAAAGAGGCTAAATTCATCTGGAAGTATGA 2159
Db 2637 CUUGGGAAGCAAGCCGCGGAAUAGUACAGAGACGUGCGGAUUCUCCAGGGAUUUUGUG 2696
Qy 2160 GCCAATATGACAATGTGGAACGGGTAGATTCACTTCTAATGCT-----CCAAA 2210
Db 2697 GCCACGAAGGACAAACGUTUAAAAACCGUUGAUUUUUAUGAUGAAUUUUUGGGAAGACCA 2756
Qy 2211 CCGGATCACACAAGAGGCTTTTATTGATGAAGGGTTTGTGTCACACCGGTTGTGTT 2270
Db 2757 CGCUGUAGUUUUAAGAGUUUAUUAUGAAGGGUUGUUGUUGAUUUAUGUUGUUGUU 2816
Qy 2271 AACTTCTGCTGCTTATCTCTGTTGCGACATCGCATACATTTACGGAGATACACAGCAG 2330
Db 2817 AAUUUUCUUGGCGAUGUCAUUGUGCGAAAUUGCAUUAUUGUUAUCCAGGACACACAGCAG 2876
Qy 2331 ATTCTTTTCAATTAACAGAGTTTCAGAATTTCCGTATCCCAACATTTTGAAGAGCTGCA 2390
Db 2877 AUUCAUACAUAUAGAUUUAUGAGUUCGCCGUACCCCGCCCAUUUUUGCCAAUUGGAA 2936

Db 3597 GAUUGCAUAUUGGAUUGCUAAGUCUGUGCGCCUAAAGGAUCAAUCAAACCAUA 3656
QY 3111 GAGCCAGTTTGTGGTACCGCGGGGAACCGCCAGGCTCGAGACTACTCGAAATCTG 3170
Db 3657 AUACCUUGUAUAGCGGGGAGAAUUGCCAGCAGACUGCAUUGGAAAUUA 3716
QY 3171 GTTGCAATGATTAAAGAAATTCACGCAACGACCTGACGGGAGCATTTGACATTTGAG 3230
Db 3717 GUGCGGAUGAUAAAGAAUUAUAAAGCAUUAUUGGCAUUAUUGAUUGAA 3776
QY 3231 AGCACCCGATCTGTTAGTAGATAAGTTTGTGATAGCTATTTTATTAAGAAAGAAA 3290
Db 3777 AAUACUGCAUUAUUGAUGAUAUUGUUAUUGAUAUUGUUAUAAAGAAAGAA 3836
QY 3291 TACACAAAATAATTGCTGGAGTGATGACGAAGGATTCATATGATGAGATGTTGGAAAC 3350
Db 3837 AAACCAAAUAAUUGUUAUUGUUAUUGAUGAGAGUCUCUAUAGAUUGUUAAGAAAG 3896
QY 3351 AGGAAAGAGTACTATTGGGACGACTTGGCTTAACCTCAAAATTTACAGATCTGCCGGCATC 3410
Db 3897 CAGGAACAGGUAACAUAUAGCCAGCUCGCAUUAUUGAUUAUUGUUAUUGGCAUUAUUG 3956
QY 3411 GATCAGTACAGACATGATCAAGGCTCAACCAAAACAGAAATTTGGACCTTTCAATTCAG 3470
Db 3957 GAUCAGUACAGACACAUGAUUAAGCAACCAAGCAAAAUUUGGACAUUCAAUCCAA 4016
QY 3471 AATGAATACCCCTGCTCTGCAAAACAATTTGCTTACCATTCGAAGCAGATCAACGGTATTG 3530
Db 4017 ACGGUAUACCGGCUUUGCAGACGAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUG 4076
QY 3531 GCCGGTTTCT--CAGAGCTTACAGAGTTGCTGCTCGAGCATTTGATTTCAAGAGTTT 3587
Db 4077 GGCCCGUUGUUAUGAGAGCUUAUAGGCAUUAUUGGACAGUGUUAUUGGAGCAUUAUUG 4136
QY 3588 CTTTTCTTTACTAGGAAACCTCAGAACAGATTCAGAAATTTTCTCGGATCTCGACTCG 3647
Db 4137 UGUUUUUUACAAGAAAGACACAGCGCAGAUUGAGAUUAUUGGAGAUUUGGAGAUUUGGAG 4196
QY 3648 CAGCTTCTGATGATGTTAGAACTGATATTTCTAAGTATGATGATGATGATGATGATGATG 3707
Db 4197 CAUUGCGGAUGAGUUGUUGGAGTUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4256
QY 3708 TTTCAATGCTGTPAGAGTATGAATATGAAAGATTGGGTCTCAATGATGATTTTGGCC 3767
Db 4257 UUCACUGUGCAGUAGAAUACGAGUUCUGCGAAGAUUGGUAUUGGUAUUGGUAUUGGUA 4316
QY 3768 GAAGTGTGGAACAGGGGACAGAAACAACTTTGAGGATTTACATTTGCTGGAATCAAG 3827
Db 4317 GAAGUUUGGAAACAGGGCAUAGAAAGACCCUUAAGGAUUAUUAUUAUUAUUAUUAUUA 4376
QY 3828 ACATGCTGTGGTATCAAGGAAAGGGGTGATGTGACTACTTTTCATCGCAATCTGTT 3887
Db 4377 ACUUGCAUCUGGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4436
QY 3888 ATAATAGCAGTTGCTTGGTTCATGTTTACCGATGAAAGAGTTCATAAAGGTGCTTTT 3947
Db 4437 AUCAUUGCUGAUUUUGGCUUUGGCUUUGGCUUUGGCUUUGGCUUUGGCUUUGGCUUUG 4496
QY 3948 TGTGGAGACGATCCGTTTGTATTTTCCAAAGGGTTTGGATTTCCCTGACATTTCACTCA 4007
Db 4497 UGCGGGAUGAUGUUGUGUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4556
QY 4008 TGTGCTAATCTCATGTGGAATTTTGGAGCCAACTGTATAGAAAGAGTACGGTTACTTT 4067
Db 4557 UCCGCGAAUUAUUGGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4616
QY 4068 TGTGGTATGATACATACATACATGATGATGATGATGATGATGATGATGATGATGATGAT 4127
Db 4617 UGCGGAAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4676
QY 4128 TTGATCTCCAACTTGGGCAAAACATATCAAGATTTATGATCACTTAGAGAGTTAAGG 4187

Db 4677 UUGAUCUCGAAACUUGUGCUAATAACACAUCAAGAUUGGAAACACUUGGAGGAGUUCAGA 4736
QY 4188 GTGCTTTTGTGCGATGTTGCTTGTTCGCTCGGAAACTGSGTCTTTAGCTTTTCGCGACGTG 4247
Db 4737 AGGUCUCUUGUGAUGUGUGUGUUCGUU--GAACAUAUUGGUGUAUUAACACACAGUUG 4793
QY 4248 AACGAGCTTATCAAGGAGTTTATAAACAAGGATTTGATGAGTTGCTTTGCTTTTAAATGT 4307
Db 4794 GACGCGCUGUAUGGGAGGUGUCAAGACCGCCUCCAGGUGUGUUGUUAUUAUUAUUA 4853
QY 4308 GTTAAACAAATTTTGTGTGATAAATTTTATTTAGAACTTTGTTTAAATGGCTGTTAG 4367
Db 4854 CUGGUAAGAUUUUGUGUGUAAGUUCUUUUUAGAAUUGUUUUUAUAGUGGCUUAGU 4913
QY 4368 TCTCAGAGATCTGTCACAAATTTAGCGAGTTTCATTGATCTTTTGGAAACAGGATGAGTACT 4427
Db 4914 UGUUAAAGGAAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4973
QY 4428 TCCGCGATTCATGACTAAGTCAAGAGTGTAGAAATATCGACTGTGGACAGATTTATGGC 4487
Db 4974 ACCGUGAUGUUUACCCUGUAAGAGUGUUAUUGUUCACAAAGUUGAUAUUAUUAUUG 5033
QY 4488 TGTTAAGAAATGATAGTCTTTCTGATGTAGATTTTACTTAAAGGTGTTAAGTTAGTTAAGAA 4547
Db 5034 UGAUGAUAUGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5093
QY 4548 AGGATATGTTGCTTACGATTTTGTGATGTTGCTGCGGAGTGGAAATCTCCCGGATAACTG 4607
Db 5094 UGGAUACGUCUGUUAAGCCUGUUGUGUCACCGGCGAGUGGAAACUUGCCUGACAAUUG 5153
QY 4608 CCGTGTGTGTGCTGATGTTTGTATTTAGTAAGAGAAATGAAAGAGAGTAAAGNAGCAAC 4667
Db 5154 CAGAGAGGUGUGAGGU 5213
QY 4668 GCTGGGTGCTATCACGCCCTCTGTCACAAAGAAATTTTCTTTTAAAGCTAATCCCTAA 4727
Db 5214 UCUGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5273
QY 4728 TTATTTCAATAACATCCGAGGATCTGAGAACGCCCTGGCAAGTGTGTAGTGAATATCAA 4787
Db 5274 UUAUGCUAUAACCAACCCAGGACGCGAUGAAACACUGUGGAAUUAUUAUUAUUAUUA 5333
QY 4788 AGAGTGGCTATGGAAGAGGATCTGCTCTTTATCTTTGGAGTTCGTTTCAATTTGTT 4847
Db 5334 AAUUGAAGAUUGCAGCGGUGUUCUGCCUUCUCUGGAGUUGUGUGUGUGUGUGU 5393
QY 4848 AGTACATAAAATAATGTAAGAAAGGTTTGGAGGAACGTAATTTTGTAGTGTGACAGACGG 4907
Db 5394 UGUUUAUAGAAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5453
QY 4908 CTCGCCAATTTGAATCACTCACTGAAAGGTTGTTGAGGAGTTCGTGAGTGAAGTACCAATGGC 4967
Db 5454 AGGCCCCAUGGAACUUAACAGAGAGAGUGUGUUAUGAUGAUGAUGAUGAUGAUGAUG 5513
QY 4968 TGTGA 4972
Db 5514 GAUCA 5518

RESULT 9

US-09-962-527-5
; Sequence 5, Application US/09962527
; Publication No. US20030049813A1
; GENERAL INFORMATION:
; APPLICANT: GARGER, STEPHEN
; HOLTZ, R. BAREY
; MCULLOCH, MICHAEL
; TURPEN, THOMAS
; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
; PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
; FROM PLANT SOURCES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:

Db 2097 GAGCAGUUCAUUAUGGCAACGGCAGAUUUCGUUAUUAUGAAGCAGAGUAGCUCUGAUUGUG 2156
Qy 1620 TACATGGCTCACTCAAAAGTTCAACAAATGAAGAACTATGTGACACAGTTTGGCAGCTTCG 1679
Db 2157 UACACGGGUCCGAUUAAGUUUAGCAAAUAGCAAAACUUUAUCGAUAGCCUGGUAGCAUCA 2216
Qy 1680 TTGTCCGCCACTGTATCAAAATCTATGCAAGTCACTAAAGATGAAGTCGGGTATGATCT 1739
Db 2217 CUUUCUGCGGUGUGCAUUCUGCAAGAUUCUCAAGAUUCUCAAGAUUCUCAAGAUUCUU 2276
Qy 1740 GATTCCAGGGAGAAAGTTGGTGTGGGATGTCATTTTGAAGAGTGCGCTCCTCAACCT 1799
Db 2277 GAAACCCGUCAAAAGUUUGAGUCUUGGAUUGCAUCUAGGAAGUGUGUUAUUAACCA 2336
Qy 1800 CGGCCCAAGGTCATTCATCGGGAGTTGTCTCGATTACAAAGGGGAAAAATGTTTACTGCA 1859
Db 2337 ACGGCCAAGAGUAGUAGUGGGUGUUGUUAAGAACCCACCGAGGAUAUAUGUGGCG 2396
Qy 1860 CTTCTATCTTATGAGAGATAGAAATGGTCACTGAGAGCGACTGGAGGAGGTGGCTGTA 1919
Db 2397 CUUUGGAAUAUGAGCAGGGUGUGUGACACUGCGAUUGGGAAGAGUAGUGUC 2456
Qy 1920 TCATCTGATCAATGTTATCTGATTTGCAAGCTCCAAATCTGAGGAAAAACAATG 1979
Db 2457 AGCUCUGAGUCUGUUGUUUAUCCGCAUGCGGGAACUCAGAACUCUCUGCGCAGACUGCUU 2516
Qy 1980 AGAGACGGTGAACCCACGCAACCTACTGCAAGATGTTGTTGATGGGTGGCTGGT 2039
Db 2517 CGAAACGGAGAACCGCAUGACUAGCGCAAGGUUUCUUGGACGGAGUUCGCGGC 2576
Qy 2040 TGTGGAAGTACAAAGAGATTTGAAAGATTTGATCTTGAAGAGATTTGATCTTGGTT 2099
Db 2577 UGUGGAAAAACCAAGAAAUUUUCCAGGGUUAAUUUGAAGAAUUAUUUAGUA 2636
Qy 2100 CTTGGAACCAAGCTGCTATGATCAGAGAGGCTTAATCATCTGCACTGATGAAGA 2159
Db 2637 CCUGGGAAGCAAGCCGCGGAUAUGAUCAGAGAGCGUGCAUUCUUCAGGGAUUAUUGUG 2696
Qy 2160 GCCAATGGAATGTGAGAACGGTAGATTCACTTCTAATGCAAT-----CCAAAA 2210
Db 2697 GCCACGAAGGACACCGUUAACCGUUAUUCUUAUGAUGAAUUUUGGGAAGACCA 2756
Qy 2211 CCGGATCACAGAGAGCTTTTATGATGAAGGTTGATGTCGACACGGTTGTGTT 2270
Db 2757 CGCUGACAGUUCAGAGGUAUUAUUAUGAAGAGGUGUUGUUGCAUCUGGUGUGU 2816
Qy 2271 AACTTCTGTGTTATCTCTGTGTCGACATCGATACATTTACGAGATACACAGCAG 2330
Db 2817 AUUUUCUGGCGAUGUCAUUGUGCGAUAUUGCAUUAUGUUAUCGAGACACACAGCAG 2876
Qy 2331 ATTCTTTTCAATTAACAGAGTTTCAGAAATTTCCCGTATCCCAACATTTTGAAGAGCTGCAA 2390
Db 2877 AUUCCAUAUCAUAUAGAUUUCAGGAUUCUGGUACCCGCCCAUUAUUGCCAAUUGGAA 2936
Qy 2391 GTGATGAAGTTGATGATGAGAGAGACACACTGATGATGCCAGGTGATGTAATTTTTC 2450
Db 2937 GUGACGAGGUGGAGACACGAGAAUUAUUAUGAUGGUGUUGCCGCGAUGUCACACAUU 2996
Qy 2451 CTACAACTCGAAGTACGAGGCGGTGACACCACTTCAACTGTACACACGATCGGTCTCA 2510
Db 2997 CUGAAGAGGAGUAUAGAGGCGUUUGUCAUGAGCAUUCUUGGUUAAAAAGUCUUGUUGC 3056
Qy 2511 TCTGATGATGAGCGGTGAGGAGTACTAAACAGTGTTCAAACCACTAAAGGGAAA 2570
Db 3057 CAGGAGUUGGCGCGGCGCGCGUGAUCAUCCGUAUCUCAAACCCUUUGCUGGCAAG 3116
Qy 2571 ATTGTAATTTCACTCAGGCTGATGAATTTGATTTAGAGGAGAGGCGTATAAGATCTG 2630
Db 3117 AUCCUGACUUUUAUCCCAUUGGAAUUAUUAUGAAGAGAGCUCUGCUUUAAGAGGUAUUCAGAUU 3176
Qy 2631 AACACCGTTATGATGATCAGAGGAAACCTTTTGAAGATGTGCTGGTTCAGATTCAGC 2690
Db 3177 CACACUGGCAUGAAGTGAAGGCGAGACAUUCUCUGAUUUUUAUUAUGUUAUUAAC 3236

Qy 2691 GCAACTCCACTGACTGTGATTTTCCAAAGTCTTCCCCGAGATGTTCTAGTCTGCTCTGACTAGA 2750
Db 3237 CUUACACCAAGCUCUCAUUGCAGGAGACAGCCCAUGUUUUGGUGCGCAUUGUCAAGG 3296
Qy 2751 CACACAAAGAGCTTCAAAATATTACACCGTAGTGTAGATCCCTTTTACAGATAAATAGT 2810
Db 3297 CACACUGUUGCUCUAAAGUACACUGUUGUUAUGGAUCCUUAUUAUGAUUAUUAUGA 3356
Qy 2811 GATTGTCTTCTTTAAAGCTCCTTTTCTTTAGAAATGTATATGTTAGAAAGCAGGTAGTAGA 2870
Db 3357 GAUCUAGAGAAACUUAAGCUCGUUAUGAUUAUGAUUAAGGUCUGAUGCAGGAACACA 3416
Qy 2871 TAGCAATTCAGATGATGAGTGTTCAAAGGTCAATATCTCTTTGTGGCAACACCTAAA 2930
Db 3417 UAGCAAUUACAGAUUGACUCGGUGUUCUAAAGGUUCCAAUUCUUUUGUGCAGGCCCAAAG 3476
Qy 2931 TCAGGAGACTTCCACATCTACAGTTCTATTACGATGTATGCTCTCCCTGCTTAATAGTACT 2990
Db 3477 ACUGGUGAUUUUCUGAUUGCAGUUUAUUAUGAUUAUGUGUCUCCAGGCAACAGACC 3536
Qy 2991 ATACTTTAAACAAAGTATGATGCTTACCATGAGGTTTACGTGATTAATAGTCTTAAATGTGAAG 3050
Db 3537 AUGAUGAUAUUUUGAUGUCGUUAUCCAGAGGUGAUGACUGACAUUAUUAUGAUGUCAA 3596
Qy 3051 GATTGTGTTCTTGATTTTTCAAAAGTATTCGATGCGCAAGGAGGTGAACCATGTCTTA 3110
Db 3597 GAUUGCAUAUUGGAUAUGUUAAGUCUGUGCGCCUAAAGGAUCAAACCAACCAUA 3656
Qy 3111 GAGCCAGTTTGGTACCGGCGGACCGCCAGGCTGCAGGACTACTCGAAAATCTG 3170
Db 3657 AUACCUAUGUAACGACCGCGCAGAAUUGCCAGCAGUCUGACUUAUUGGAAAAUUUA 3716
Qy 3171 GTTGCATGATTAAGAAATTTTCAACGCCACAGACTGACGCGGACGATTTGACATTGAG 3230
Db 3717 GUGCGGAGUAUAAGAAACUUAUACGACCCGAGUUGUCUGCAUCAUUAUGAUUGAA 3776
Qy 3231 AGCACCGCATCTGTTGATGATAAGTTTGTGATGATTTTATTTATAAAAAAGAAAA 3290
Db 3777 AAUACUGCAUCUUUAGUUGAUAAGUUUUUUUUGAUAUUAUUGCUUUAAGAAAAAAGA 3836
Qy 3291 TACACAAAAAATTCGTGAGTGATGACGAAGGATTTCAATGATGAGATGTTGGAAAAAC 3350
Db 3837 AAACCAAAUAAAAGUUUCUUGUACUAGUAGAGUCUCUCAUUAUGUUAUUAAG 3896
Qy 3351 AGGAAAGAAAGTACTATTGGACGACTTGGGTAACTACAATTTTACAGATCTGCGCGCATC 3410
Db 3897 CAGGAACAGGUAACAAUAGSCCAGCUGCAGAUUUUUAUUAUUAUUGCCAGCAGUU 3956
Qy 3411 GATCAGTACAGACATGATCAAGGCTCAACCAAAAACAGAAATTTGACCTTTCAATTCAG 3470
Db 3957 GAUCAGUACAGACACAUUAAGCACAACCCCAAGCAAAAUUGGACACUUCAAUCCAA 4016
Qy 3471 AATGAATACCTCTCTCGAAAAAATTTGTCTACATTTGAAAGCAGATCAACGGTATTTTG 3530
Db 4017 ACGAGUACCCGCGUUUGCAGAGAUUGUGUACUUAUUAUUAUUAUUAUUAUUAUUA 4076
Qy 3531 GCGGTTTCTCT--CAGAGCTTACAAGGTTGCTGCTCGAGGCATTTGATTTCTAAGAAGTTT 3587
Db 4077 GGCCCGUUAUGAGGCUUAUAGGCAAUUACUGGACAGUGUUGAUUUGCAGCAGAUUU 4136
Qy 3588 CTTTTCTTTTCTAGGAAAACTCCAGAAACAGATTTCAAGAAATTTTCTCGGATCTCGACTCG 3647
Db 4137 UUGUUUUUACAAGAAAGACACGAGCGCAGAUUGGAGAUUUUUCUGGAGAUUCUCGACAGU 4196
Qy 3648 CAGTTCTCTATGATGTTGTTAGAACTGGAATTTTCTAAGTATGATAGTACAGAAACGAG 3707
Db 4197 CAUGGCGGAGUAGUUCUUGGAGUGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4256
Qy 3708 TTTCTATGTTCTGATGATGAATATGAAAGATTTGGGTCTCAATAGATGATTTTGGCC 3767
Db 4257 UUCACUGGCAUGAUAACGAGAUUCUGGCGAAGAUUGGUGUUUUAAGAAACUUCUUGGGA 4316

Db	597	GCUGUCUGUACAAUACUUCAGACAAUCCGCAUCCAGCGCAUGCAGCAUACAGGCGA	1677	GCUCUGUGGCAUGCCUGGCUUGACAUUAGGAAGAAUGAAGAAACGGAAGUGAUG	1736
Qy	126	AGATACGCTGTGCTCTGACAGTGTGTATGATATCTCTTAAAGGGTGTGATATATTTTCGATATCGGAAG	1206	TACGACGCGTTATCAGAAATATCTATCTCTTAAAGGGTGTGATATATTTTCGATATCGGAAG	1265
Db	657	GUGUUGCCAUUGGCUACACAGCAUAUAGCAUACACCGCGGAUGAGUUCGGGCGGCA	1737	UACAAUGCAUUCACAGAUUACGGUGUUAAGGGAGUCUGACAAAUUCGAUUGUUGAUUU	1796
Qy	186	TTAATATCTAAGAAATAPACATGATGATGTTATGCGAGTTCCTATTTGGCAGAAGCATATTA	1266	TTCAAAGACATGTGCAAGGCTTTAGATGTAGTCTCTGATGTGCGCACGACGATTAATCGTT	1325
Db	717	CUCUUGAGGAAAAUUGCAUAGUGUCCGCUUUCUCCAUUCUCUGAGAAACCGUCU	1797	UUUCCCAUGAUGGCCAAUCUUUUUAGGAAUGACCAAUAGCGCAGCAAGAAUUUAUAGU	1856
Qy	246	CTAGACCAAGCGAGGTTCGCTTAATGAATAGGCGCACTTTCAAAAGAGAGGTGAT	1326	GCAGTGCGCGAGAAATAGAAGCGGTTTAACTCTTACTTTTATAGCAACCGCAGGAGAAAT	1385
Db	777	CUTGAAGAUCAUCGCUAAUUGGACGAAUACAACCGUGUUUUCGCGCGGAGAGAC	1857	GCUGUCAUGACAAUGAGAGCGGUCUGACUCUCAUUAUUGAACGACCUACUGAGCGCAU	1916
Qy	306	GATGTTCTTTCTTTCTTGCTGATGAAGTACTTTAAATATATAGTCAATAATACAAAAAT	1386	GTGGCTAAGGCTCT-----TAAAGCACGGCGTCTGAGGCCGTGTATCTTTGAACCG	1439
Db	837	AAGUAGACUUUUUUUGCAUCAGAGAGUUCUCUUAUUAUUGUCAUUAUUCUUAU	1917	GUUGCGCUAGCUUUAACAGNAUCAAGAGAGGCUUCAGAGAGGUGCUUUGUAGUUAUCCUCA	1976
Qy	366	ATCTTGCAATTATGATGATTAATCTTACTTTCTGCTTCTAGTAGAAATAGTTTACTTTAAG	1440	ACATCCGAAGAGGTGAACGTAATAATTTTCTATTGCTGAGAAAGGAGATTGCGCTGTG	1499
Db	897	AUUCUUAAGUUGUGCAAAAACUUAUCUCGCGCCUCUAAUAGAGAGGUUAUCAUGAAG	1977	AGAGAAUGUAGAAGAACCGUCCAUAGAAGGGUUCGAUGGCCAGAGAGAGAUUACAUAUAGCU	2036
Qy	426	GAATTTTACTACTAGGTTAATACTTGTGTTTGTAAATTTACCAAGTAGATACCTAT	1500	TGTGCGAGAAAGTCATGTTTTCAGCAATGCTTAACTTAGAGCACGAGAGTTGGAGTCCCTC	1559
Db	957	GAGUUUUUAGCACCAGAGUUAUACCGUGUUUUGAUGUUUUCUAGAAUAGAUUUU	2037	GGUUCUGGAGAUCAUCCGAGUCGUCUUAUUAAGNACCGAGAGAUAGAGUCUUUA	2096
Qy	486	ATTCTGTAAGAAGTGTGTACAAAGTAGGCTGTGATAGTATGATCTTCTATGAGCGCATG	1560	AACGATTTTCCATAAGCTTTGCGTGGATGTGTTGATTACAAAGCAAAATGGCATCGTGTGTC	1619
Db	1017	CUUUUGUACAAGGUGUGGCCCAUAAAGUGUAUGAUGAGUCAGUUUAUACUGCAUUG	2097	GAGCAGUUUACUUAUGGCAACCGGCGAGAUUCGUUAUUCGUAAAGCAGAGAGCUGCAUUGUG	2156
Qy	546	GAGAGCGCTTGTGTTACAGAAAAACCTTGCGCATGTTCAACACTGAAAGAGCAACTTTT	1620	TACACTGGCTCACTCAAGTTTCAACAAATGAAGAACTATGTGCGACAGTTTGGCAGCTTCG	1679
Db	1077	GAAGACGCAUGCAUUAACAAAAAGACUCUUGCAUUGGCAACGCGCAGAGAAUCCUCCU	2157	UACACGGGUCGAAUAAAGUUCAGCAAAUGAAAAAUCUUUACGAUAGCCUGGUGAGCAUCA	2216
Qy	606	AGAGACCGCTTCGTTTACTTTTGTTCCTTAAGATGAAGACATGTTGATAGTACCG	1680	TTCTCGCCACTGTATCAAAATCTATCAAGTCTACTAAAGGATCAAGTTCGGGTATGATCT	1739
Db	1137	GAGGAUUAUCAUGACUACAUAUACUGGUUCCCAAAUGAGGGAUUGGUAUGGUAACCA	2217	CUAUUCUGCGGUGUGGAUUCUGUCNAGAUCCUACAAGUACAGCUGCUUAUUGACCUU	2276
Qy	666	CTGTTTGAGGGTTCATTACAGCAAAAGATGACAAAGGAGTGAAGTCAATGTTAATCGT	1740	GATTCCAGGAGAGAAAGTTGGTGTGGGATGTCACTTTTGAAAAAGTGGCTCTCTCAAACT	1799
Db	1197	UUAUUCGACAUUCUUGGAGACUAGUAAGAGGACGCGCAAGGAUUGUUGUCCAG	2277	GAACCCGCUAAAAUUGUGAGUCUUGGAGUUGUCAUCUAGGAAGUGGUUAUACCAACCA	2336
Qy	726	GACTTCGTTTACAGTGTCTTAATCATATCAGAAATATCAAGCAAAAGCGTTTAACCTTAC	1800	GGCGCCAAAGGTCATTCATGGGAGTTGTCTCTGGATTACAAGGGGAAAAATGTTTACTGCA	1859
Db	1257	GAUUCUGUUAACAGUGCUUAACCAUUCGAACAUACAGCGCAAAAGCUCUUAUAC	2337	ACGCGCAAGAGUCACUAGGUGGUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUG	2396
Qy	786	CAGAACGTATATCTTCTGAGTCTATAAGATCCCGCTGATATCAATCAATGTTGTTACT	1860	CTTCTATCTTATCAAGGAGATAGATGGTGTGACCTGAGAGCGACTGGAGAGGGTGGCTGTA	1919
Db	1317	GCAAAUGUUUGUCCUUGCAUUCGAUUCGAUUCGAGGGGUAUUAUUAACGGUGUGACA	2397	CUUUGGAUUAUGAGCAGGAGGUGUGUGACAUUGCGAUUUGGAGAGAGUAGCUGUC	2456
Qy	846	GCTAGGCTGAATGGGATGTAGATAAAGCAATCTTCAACCCCTGTCAATGACTTTCTTC	1920	TCACTGATACAATGGTATATCTGATATTTGCAAAAGCTCCAAATCTGAGAAAAACAATG	1979
Db	1377	CGAGGUCCGANAUGGGAUGGACAAUUCUUGUUAUUAUUCUUGUCCAUUGAGCUUUUAC	2457	AGCUCUGAGUCUGUUGUUAUUCGCAUGGCGCAAAACUCAGAACUCUCGCGCAGACUCU	2516
Qy	906	TTGCAGACTAAGCTGGCTGCGCTTCAAGACGATATAGTAATGGAAGAAAGTTTCGGTGTG	1980	AGAGACGCTGAACCCACGACCTACTGCAAGATGCTACTTGTGGATGGGTGCGCTGCT	2039
Db	1437	CUGCAUACUAAAGCUGUCCUUAAGGAUGACUUAUCUGAUUAGCAAGUUAUUGUCUGU	2517	CGAAACGGAGAACCGCAUGUCAGUAGCGCAAAAGGUUUGUUGUUGUUGUUGUUGUUGUUGU	2576
Qy	966	GATAGACCACTCTGCACTTATTTGGGATGAGTGGGCAAAATTTTGGAAAGCTTTTC	2040	TGTGGAAGATFACAAAGGAGATTTTGAAGATTTGATCTTCTGATGAGGATTTGATCTTGGTT	2099
Db	1497	UCGAAAAACGGUGCCAGCAUGUGUGGAUGGAUUCGUGGUGUUUUGGGAACGCAUUU	2577	UGUGGGAACCAAGAAAUUCUUCAGGGAUUAUUUUGAUGAAGAUCAUUAUUUUGAUA	2636
Qy	1026	CCCACTATCAAGAGAGATGGTGAGCAGGAAAAATCTGGATGTAAAGTGAAGATGCTCTG	2100	CTTGGAACAACAGCTGCTGTATGATCAGAAAGGCTTAATTCATCTGACTGATAGA	2159
Db	1557	CCUCCUGGAAGAGAGGCUUGAACAGGAAACUUAUCAGAGUGGCGAGCGCAUAUA	2637	CCUGGGAAGCAAGCCGGAUUAUGACAGAAAGCUGGCGAAUUCUCAGGGAUUAUUGUG	2696
Qy	1086	AAGATCAAGATCCAGATCTGTATGTCAATGGAAGACAGAGTTTCGTAGCTGAATACCC	2160	GCCAATATGACAAATGTGAAACGCTAGATCTTCTTCTTAATGCTATCTTCTTCTTCTTCT	2210
Db	1617	GAGAUCAAGGGUGGUGAUCAUUAUGUAGACCUUCCACGACAGAUUAGUGACUGAGUACAAG	2697	GCCAGAGAGACAAACGUUAAAAACCGUUUUAUUUUUUGAUGAUAUUUUGGGAAGACACA	2756
Qy	1146	AAGTCTCAGAGGTTTACCGCATCTAGATATCAAGAAGGACTTTAGAAAGAGCTTGAGCAATG	2211	CCGCGATCACAAGAGGCTTTTATTTGATGAAGGGTGTGATGCTGCAACCGGTTGTGTT	2270
			2757	CGCUGUCAGUUAAGAGGUUAUUAUUGAUGAAGGGUUGAUGUUGCAUCUGGUUGUGUU	2816


```
Db 4974 ACCGUGAUGUUAACCCUGAAGAGUGUUAUGUUCACAAAGUUAUAAUAAUAAUGGU 5033
Qy 4488 TGTTAAGAAATGATAGTCTTCTGATGATAGATTTACTTTAAAGGTGTTAAGTTAGTTAAGAA 4547
Db 5034 UCAUGAAGUAGUCAUUGUCAGAGGUGAACCUUUAUAAAGGAGUUAAGCUUAUGAUAG 5093
Qy 4548 AGGTATGTGTGTTAGTGAATGTTGTTAGTGTCTGGGGAGTGAATCTCCCGAATAGT 4607
Db 5094 UGGAUACGUGUUAAGCGGUGUGUCGACGGCGAGTGGAAACUUGCCUGACAAUUG 5153
Qy 4608 CCGTGGTGTGTCAGTCTTGTATTGTAGATAGAGATGAAAGGAGTAGAGGACCAAC 4667
Db 5154 CAGAGGAGGUGAGCGUGUGUCUGGUGACAAAGGAAGGAAAGACCGACGAGCCAC 5213
Qy 4668 GCTGGGTGCGGTATCACGCCCTGCTTGCACAAAAGAAATTTCTTTTAAAGCTAATCCCTAA 4727
Db 5214 UCUGGUAUCUUAUACACAGCAGCUGCAAGAAAGAAUUAUCAGUUAAGGUGUCCAA 5273
Qy 4728 TTATTCAATCAATCCAGAGATGCTGAGAAGCACCCGTGGCAAGTGTGTAGTGAATACAA 4787
Db 5274 UUAUGCUUAUAAACACCCAGGACGCGAUGAAAAACGUCUGCAAGUUUUAAGTUAUUAUAG 5333
Qy 4788 AGGAGTGGCTATGGAAGAAGATGCTGCTTTATCTTTGAGTTCGTTTCAATTTCTGT 4847
Db 5334 AAUGUGAAGUGUCAGCGGUGUUCUGCCUGUUCUGGAGUUUGUGUGCGGUGUGU 5393
Qy 4848 AGTACATAAAAAATGTAAGAAAAGGTTTGGAGGAAACGTTATTTTGAGTGTGACAGCGG 4907
Db 5394 UGUUAUAGAUAUAAUUAUUAUAGUUUGAGAGAGAAUUAUAAACGUGAGAGACGG 5453
Qy 4908 CTGCGCAATTGAATCACTGAAGAAGTGTGTGAGGAGTTCTGTGATGAATGCAATGGC 4967
Db 5454 AGGCCCCAUGGAAUUAACAGAGAAGUGUGUAGAGUUAUGGAGAGUUGCCUUAUGUC 5513
Qy 4968 TGTGA 4972
Db 5514 GAUCA 5518
```

RESULT 11

```
US-09-962-527-4
; Sequence 4, Application US/09962527
; Publication No. US20030049813A1
; GENERAL INFORMATION:
; APPLICANT: GARGER, STEPHEN
;             HOLTZ, R. BARRY
;             MCULLOCH, MICHAEL
;             TURPEN, THOMAS
; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
;                     PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
;                     FROM PLANT SOURCES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING APPLICATION NUMBER: US/09/962,527
; FILING DATE: 24-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/037,751
; FILING DATE: 10-march-1998
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Halluin, Albert P
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 00801.0140.999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-463-8109
; TELEFAX: 650-463-8400
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6475 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
; US-09-962-527-4
;
; Query Match 40.8%; Score 2031; DB 10; Length 6475;
; Best Local Similarity 44.4%; Pred. No. 0;
; Matches 2212; Conservative 957; Mismatches 1795; Indels 21; Gaps 4;
;
; Qy 6 AAGGTAATTCCTGAGTTTCAAAGGAGGCTTTTAAACAGGTATGCAGAAGCTCCCAAGCAA 65
; Db 537 AAAACAGUCCCAACUUCCAAAGGAAGCAUUAUGACAGAACGACAGAAAUUCCUGAAGAC 596
; Qy 66 GTCGTGCTCTTAAACTTTTCAGGATTGTCGAATACATCCGCCAGAGATAGTGGTAGA 125
; Db 597 GCUGUCUGUCACAAUACUUCAGACAAUUGCGCAUUGCCGAUGCAGCAUACAGGCGAGA 656
; Qy 126 AGATACGCTGTTCTCTGACACAGTTTGTATGATATTCCTGTGATGAGTTTGGAGCTGCG 185
; Db 657 GUGUUGCCAUUGCGUACACACAUUAUGACAUACACCGCCGAUGUUGGGGGCGCA 716
; Qy 186 TTAATATCTAAGAATATACATGATGTATGTATGAGTCTTCATTTTGGCAGAAGCATTTATTA 245
; Db 717 CUCUUGAGGAAAAUUGUCCAUACGUGCAUUGCCGCUUCCAUUCUCUGAGAACCCGCUU 776
; Qy 246 CTAGACCAGCGGAGGTACGCTTAATGAATAGGCGCACTTTCAAAGAGAGAGGTGAT 305
; Db 777 CUUGAAGAUUACUACGCUAAUUGGACGAAUUAACACGCGUGUUUUUUGCGCGAUGGAGAC 836
; Qy 306 GATGTTTCTTTTCTTGTGATGAAAGTACTTTTAAATATATAGTCATAAATACAAAAAT 365
; Db 837 AAGUGACCUUUUUUUGCAUCAGAGAGUACUUAUUAUUGCAUUAUUGCAUUAUUCUAU 896
; Qy 366 ATCTTGCAATTATGATTAATCTTACTTTCTGCTTCTAGTGAATAGTTTACTTTTAAG 425
; Db 897 AUUCUUAAGUUGUGUGCAAAAACUUAUUCGCGCCUUAUUAUAGAGAGAGUUAUUAUAG 956
; Qy 426 GAATTTTGTAGTCACTAGGTTTAACTTCTGCTTTTGTAAATTTTACCAAGTAGATACCTAT 485
; Db 957 GAGUUUUUAGUCACACAGAUUAUACUUGUUUUUUAUUGUUUUUUAUUAUUAUUAUUAU 1016
; Qy 486 ATTCTGTACAAGAGTGTTAGACAAGTAGGCTGTGATAGTGTATGATGAGCGCATG 545
; Db 1017 CUUUUUAACAAGGUGUGGCCCAUAAAGUUAUAGUAGUAGAGAGAGUUUUUAUUGCAUUG 1076
; Qy 546 GAAGACGCTTTGCTTACAAGAAAAACCTTGCGCATGTTTCAACTGAAAGAGCAATCTTT 605
; Db 1077 GAAGACGCAUGGCAUUAUAAAAAGACUUCUUGCAUUGGCAACACGCGAGAGAAUUCUCCU 1136
; Qy 606 AGAGACACGCTTTCGGTTTAACTTTTGTCTTCCCTTAAGATGAAGGACATGGTGATAGTACCG 665
; Db 1137 GAGAUUAUACUACAGUCAAUUAUACUGUUUUUCCCAAAUAGAGGAGUUAUUGUUAUUAU 1196
; Qy 666 CTGTTTGGAGGTTCTATTACCAAGCAAAAGATGACAGAGGAGTGGGTCATTGTTTAAATCGT 725
; Db 1197 UUAUUCGCAUUAUUGGAGAGUUAUAGAGAGGCGCGCAAGGAAGUUAUUGUUGUCCAAAG 1256
; Qy 726 GACTTCGTTTACAGTGTCTTAATCATATCAGAACATATCAAGCCAAAGCGTTTAACTTAC 785
; Db 1257 GAUUCGUGUUUAACAGUGCUUAACCAUUCAGAAUACCAUUCAGGCGGAAAGCCUUAUAC 1316
```


MCULLOCH, MICHAEL
TURPEN, THOMAS

TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
FROM PLANT SOURCES

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/828,029
FILING DATE: 20-Apr-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/962,527
FILING DATE: 24-Sep-2001
APPLICATION NUMBER: 09/037,751
FILING DATE: 10-march-1998
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P
REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET NUMBER: 00801.0140.999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109
TELEFAX: 650-463-8400
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6475 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: Genomic RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-828-029-4

Query Match 40.8%; Score 2031; DB 19; Length 6475;
Best Local Similarity 44.4%; Pred. No. 0;
Matches 2212; Conservative 957; Mismatches 1795; Indels 21; Gaps 4

Qy 6 AAGGTAATCTCGAGTTTCAAGGAGCGCTTTAAACAGGTATGCAGAGCTCCCAACGAA 65
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
537 AAAACAGUCCCCAACUUCCAAAGGAAGCAUUUGACAGAUGCAGACAUCUGAAGAC 596
Qy 66 GTCTGCTGCTCTAAACATTTTCAGGATTTGTCCAATAACATCCGCCAGAGAAATAGTGTAGA 125
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
597 GCUGUCUGUCAUAUCCUCCAGACAUCGCGAUCAGCCGCGAUCAGCAUUCGGGCGCA 656
Qy 126 AGATACGCTGTTGCTCTGCACAGATTTGATGATATTTCTGTGCATGAGTTTGGAGCTGGC 185
Db :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
657 GUGU AUGCCAUUGCGCUACACAGCAUAU AUGACA UACCAGCCGCGAUGAUUCGGGGCGCA 716
Qy 186 TTAATATCTAAGATATACATGTATGTTATGCAGCTTCCATTTTGGCAGAAGCATTTATTA 245
Db :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
717 CUUUGAGGAAAUAUGUCCAUAGCGUCGUAUGCGGUUUCACUUCUUGAGAACCGUUCU 776
Qy 246 CTAGACACAGACGGAGGTTTACGCTTAATGAAATAGGCGCAACTTTCAAAAGAGAAGGTGAT 305
Db :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
777 CUUGAAGAUCAUACGUCAAUUUGAGCAAAUACAACGCGGUGUUUUCGCGGAUGGAGAC 836
Qy 306 GATGTTTCTTTTTCTTGCTGATGAAGAGTACTTTTAAATATAGTCATATAATACAAAAAT 365
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
837 AAGUUGACUUCUUCUUUGCAUCAGAGAGUACUCUUAAUUAUUGCAUAGUUAUUCUAAU 896
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

1977	AGAGAGTUGAAGAACCGGUCUCCAGUAGGGUUCGUAUGCCGACAGAGAGAGUUA	2036	
1500	TGTCGACGAAGTCTATGCTTTTGACGAATGCTAACTTAGAGACACACGAGAGTTTGGAGTCCCTC	1559	
2037	GGUCUCUGGAGAGUAUCAUGCGGAGUCGUCUUAUUCUAAAGAACGAGGAGUAGAGUCUUUA	2096	
1560	AACGATTTTCATTAAGGCTTGCGTGGATAGTGTGATTACAAAGCAAAATGGCATCGGTTGTC	1619	
2097	GAGCAGUUUCAUUGGCCAACCGGCAGAUUCGUUAAUUCGUAGAGACGAGUCUGAUUGUG	2156	
1620	TACACTGGCTCACTCAAAGTTTCAACAAATGAAGAACTATGTGCACAGTTTGGCAGCTTGC	1679	
2157	UACACGGGUCGCAUUAUAGUUCAGCAAAUAGAAAAACUUUAUCGAUAGCCUGGUGAGCAUCA	2216	
1680	TTGTCCGCCACTGTATCAATCTATGCAAGTCTCAATAAGGATGAAGTTCGGGTATGTTCT	1739	
2217	CUAUCUGUCGGUGUGCAUUCGUAUGGUAUCCUAAAGAUCCAGCUGCUAUUUGACCUU	2276	
1740	GATTCCAGGGAGAAAGTTGGTGTGTTGGGATGTCTACTTTGAAAAAGTGCCTCTCAAACTT	1799	
2277	GAACCCGUCNAAAGUUGGAGUCUUGGAGUUGCAUUAAGGAGUUGUUAUCNAAACCA	2336	
1800	CGGCCAAAGGTCATTCATCGGGAGTTGTCTCTGGATTACAAAGGCGAAAAATGTTTACTGCA	1859	
2337	ACGCCAAGAGUCAUGCAUGGUGGUGUGUUGUAAAAACCCACGCGAGAAUUAUUGUGCGC	2396	
1860	CTTCTATCTTATGAAGGAGATAGAAATGGTGACTGAGAGCGACTGGAGGAGGTGGCTGTA	1919	
2397	CUUUUGAAUUAUGAUGAGCAGGGUGUGUGUCAUGCGAUGAUUGGAGAAAGAGUAGUCUG	2456	
1920	TCATCTGATACAATGGTATATCTCGATATTGCAAAAGCTCCAAAATCTCGAGAAAAACAATG	1979	
2457	AGCUCUGAGUCUGUUGUUUAUUCGACAUGGCGGAAACUCAGAACUCUGCGCAGACTGCUU	2516	
1980	AGACACGGTGAACCCCAACGAACTTCTGCAAAAGATGTACTTTGTGGAATGGGGTGCCTGGT	2039	
2517	CGAAACGGAGAACCGCAUCAGUAGCGCAAGGUGUUCUGUGGACCGAGUUCCGGCG	2576	
2040	TGTGGAAAGTACAAGGAGATTTTGAAGATTTTCATCTTGATGAGGATTTGATCTTGGTT	2099	
2577	UGUGGGAACCAACGAAGAAAUUUUCAGCGGUGUAUUUUGAUGAAGAUCAUUUUUAGUA	2636	
2100	CCTCGAAAAACAGCTGCTGTATGATCAGAAAGAGGCTAATTCATCTGACACTGATAAGA	2159	
2637	CTUGGGAACGAAGCCGCGGAAUUGAUCAAGAAGCUGGCGAAUUCUUCAGGGAUUUUGUG	2696	
2160	GCCCAATTGGCAATGTGAGAACCGGTAGATTCACCTTCTAATGCAAT-----CCAAAA	2210	
2697	GCCACGAAGGACAACGUUAAACCGUGAUUUUCAUGAUAUUUUUGGAAAAAGCACCA	2756	
2211	CCGGATCACACAAGAGCTTTTATTGATGAAGGGTTGATGCTGTCACACCGGTTGTGTT	2270	
2757	CGCUGUCAGUUCACAAGAGUUAUUAUUGAUGAAGGGTUGAUGUUGUUGCAUCUGGUGUGU	2816	
2271	AACCTTCGTGTGCTTATCTCTGTTGGACATCCCATACATTTTACGAGATACACACAG	2330	
2817	AUUUUUUGUGGCGAUGUCUUAUGUGCGAAAUUGCAUUAUGUUUUAACGAGACACACAG	2876	
2331	ATTCTTTTCATTAAACAGAGTTTCAGAAATTTCCGTTATCCCAACCAATTTTGGAGAAGCTCAA	2390	
2877	AUCCCAUACAUAUAGAGUUUCAGGAUUCCGUACCCCGGCCCAUUUUUGCCAAAAUGGAA	2936	
2391	GTGGATGAAGTTGATGAGAGGAGGACCACTGTAGATGCCAGGTGATGTGAATTTTTTC	2450	
2937	GUUGACGAGGUGGAGACGACGAGAAACUACUCUCUGGUGUCGCGGAGUUCACACAUU	2996	
2451	CTACAATCGAAGTACGAAGGAGCGGTGACCAACTTCAACTGTGTACAAACGATCGGTCTCA	2510	
2997	CUGAACGAGAGAUUAGAGGGCUUUGUCAUGAGCACUUCUUCGGUUUAAAAGUCUGUUCG	3056	
2511	TCTGAGATGATAGGCGGTAAAGGAGTACTTAAACAGTGTTCCTCAAAACCACTAAAAAGGAAA	2570	

3057	CAGGAGAUGUUGCGGGAGCGCCGCCGUAGUAUCAUCCGAUCUCAAACCCUUUGCAUGGCNAG	3111
2571	ATTGTAACTTTTCACTCAGGCTGATAAATTTTGAGTTAGAGGAGAAGGCTATAGAATGTG	2630
3117	AUCCUGACUUUAACCNAUCGGAAUAAGAAGCUCUCUUCRAAGAGGUAUCAGAUUU	3176
2631	AACACGGTTCATGAGATCCAAGGAGAAAACCTTTGAAGATGTGTGCTGGTCAGATTGACG	2690
3177	CACAUCUGCAUGAAGGCAAGCGAGACAUAUCUCUGAUGUUUCACVAGTUAGGUUAACC	3236
2691	GCAACTCCACTGACTGTGATTTCCAAGTCTTCCC CGCATGTTCTAGTCGCTCTGCATCAGA	2750
3237	CCUACACCCAGUCUCCAUCAUUGCAGGAGACAGCCCAUGUUUUUGGCUUUGCAUUGAACG	3296
2751	CACACAAAGAGCTTCAAAATATTACACGTAAGTCTTAGATCTCTTTAGTACAGATAATTAGT	2810
3297	CACACCUUGUCUGAAGUACUACA CUGUUGUUAUGNAUCCUUAUGUUAUGAUCAUUA	3356
2811	GATTTGTCTTCTTTAAGCTCTCTCTTTTAGAAAAATGTATATGTGTAGAAGCAGGTAGTAGA	2870
3357	GAUCUAGAGAAAACUAGCUGCUCUACUUGUUAUAUUGUUAAGGUCGAUGCAGGAACACAA	3416
2871	TAGCAATTACAGATGATGCAGTGTCCAAGSTCATTAATCTCTTTGTGGCAACACCTTAA	2930
3417	UAGCAAUUACAGAUUGACUCGGUUGUCAAAGGUUCAAUCUUUUUGCGCGCCNAAG	3476
2931	TCAGGAGACTTTCAGACTCACAGTTCATTACAGTGTATGCCCTCCTCGTGAATAGTACT	2990
3477	ACUGGUAUUAUUCUGAUAUGCAGUUUAUCUAUGAUAUGUCUCCAGGCACACGACC	3536
2991	ATACTTAAACAGTATGATGCTGTTTACATGAGGTTACGTGATTAATAGTCTTAAATGTGAAG	3050
3537	AUGAUGAAUAAUUUGAUGCUGUUA CCAUGAGGUGUACUGACAUUUAUGAUAUGUCAA	3596
3051	GATTTGTCTTCTGATTTTCCAAAAGATTTCCGATGCCAAAGAGGTTGARAACCATGCTCTA	3110
3597	GAUUGCAUAUUGCAUAUGUUAAGUCUGUUGUGCGCCUUAAGGAUCAAAUCAAACCAUA	3656
3111	GAGCCAGTTTGTGCTACCGCGCGGGAACCCCAAGGCTGCAGAGCTACTTCGAAAATCTG	3170
3657	AUACCUUGUUAAGAACGGCGGCAGAAAUGCCACGCCAGACUGGACUAUUGGAAAAUUUA	3716
3171	GTTCGAATGATTAAGAANAATTTCAACGCACACAGACCTGACGGGAGCGATTGACATTGAG	3230
3717	GUGCGGAUGAUAAAAGGAACUUUAACGCACCCGCGAGUUGUCUGGCAUCAUUGAUUAUGAA	3776
3231	AGACCCGCACTGTTGTAGTAGTAAGTTTTTTTGTATGACTATTTTATTA AAAAGRAAAA	3290
3777	AUAUCGCAUCUTUUGUUGAUAAGUUUUUUGAUAUUAUUUUUUAAGAAAAAAGA	3836
3291	TACACAAAAATATGTCTGAGTGATGACGAAGGATTCAAATGATGAGATGGTTGGAAAAAC	3350
3837	AAACCAAAUAAAAGUUUUUUGUUCAGUAGAGAGUCUCUCAUAUGAUGUUAGAAAAG	3896
3351	AGGAAAGAAGTACTATTGGACGACTTGGCTTAACTACAATTTTACAGATCTGCGGCGCATC	3410
3897	CAGGAAACAGGUAAACAAUAGCCAGCUGCGCAGAUUUUGAUUUUUGCAUUGGCCAGCAGUU	3956
3411	GATCAGTACAAGCACATGATCAAGGCTCAACCCAAAACAGAAAATTTGGACCTTTCATTTGAG	3470
3957	GAUCAGUACAGACAUGAUUUAAGCAACAACCCAGCAAAAUAUUGGACAUUCAAUCCAA	4016
3471	AATGAAATACCTGCTCTGCAAAACAAATGTCTACCATTCGAAGCAGATCAACGGTATTTTG	3530
4017	ACGGAGUACCGGCUUUGCAGACGAUUGUUAACCAUUCAAA AAAAGCAUUGCAAAUUU	4076
3531	GCCGGTTCT---CAGAGCTTACAAGGTTGCTGCTCGAGGATTTGATTTCTAAGAAGTTT	3587
4077	GGCCCGUUGUUUAGUGAGCUUAUAGGCAAAUUAUGACACAGUGUUAUUGCGACAGAUUU	4136
3588	CTTTTCTTTACTAGGAAAATCCAGAACAGATTCAGAAATTTTTTCTCGGATCTCGACTCG	3647
4137	UUGUUUUUCCACAGAAAGACACCAAGCCGACAGUAGGAGUUUUUUCGGAGAUUCGACAGU	4196

Db 837 AAGTTGACCTTTCTTTGGATCAGAGAGTACTCTTAATTAATGTCATAGTTATCTAAT 896
Qy 366 ATCTTGCAATTATGATGAGTAAATCTTACTTTCTGCTCTTAGTAGAAATAGTTTACTTTAAG 425
Db 897 ATCTTAAGTATGTCGCAAACTTACTTCGCGSCCTCTAATAGAGAGGTTTACATGAAG 956
Qy 426 GAATTTTATGACTAGGTTTAATACCTTGGTTTGTGTAATTTACCAAAAGTAGATACCTAT 485
Db 957 GAGTTTTTATGTCACAGAGTTAATACCTGTTTTGTGAAGTTTTCTAGAATAGATACTTTT 1016
Qy 486 ATCTGTACAGAGTGTGACAGAGTAGTGGTGTGATAGTATGATCATGTTCTATGAGCGCATG 545
Db 1017 CTTTTGTACAAAGGTGTGGCCCATAAAGTGTAGATAGTGAAGTTTTTATCTGCAATG 1076
Qy 546 GAAGACGCCCTTTGCTTACAGAAAACCTTGGCCATGTTCAACACTGAAAGAGCAATCTTT 605
Db 1077 GAAGACGCATGGCATTACAAAAGACTCTTGCAATGTGCAACAGCGAGAGAACTCTCCTT 1136
Qy 606 AGAGACACGGCTTCGGTTAACTTTTGGTTCCCTHAAGATGAAGACATGGTGTATGATACCG 665
Db 1137 GAGGATTCATCATCAGTCAATTACTGTTTTCCCAAAATGAGGGATATGGTCATCGTACCA 1196
Qy 666 CTGTTTCAGGCTTCTATTACAGCAAAAGATGACAAGGAGTGAGGTCATTGTTAATCGT 725
Db 1197 TTATTCGACATTTCTTTGGAGACTAGTAAGAGGACGCGAAGGCTTCTAGTGTCCAAG 1256
Qy 726 GACTTCGTTTTACAGTGCCTTAATCATATCAGAACATATCAAGCCAAAGCGTTAACTTAC 785
Db 1257 GATTTCTGTTTACAGTGCCTTAACCAATTCGACATACACAGCGGAAAGCTCTTACATAC 1316
Qy 786 CAGAACGTATATCTTTCGGTGGAGTCTAATAGATCCCGCGTGATGAATCAATGTTGTTACT 845
Db 1317 GCAAAATGTTTTGTCCTTTGTCGAATCGATTCGATCGAGGGTAACTCAATAACGGTGTGACA 1376
Qy 846 GCTAGGCTCAAGTGGGATGTAGATAAAGCAATCTTCAACCTTGTCAATGACTTTCTTC 905
Db 1377 GCGAGGTCGGAATGGGATGTGACAAATCTTTGTTAACAATCTTGTCCATGACGTTTTAC 1436
Qy 906 TTGCAGACTAAGCTGGCTGGCTTCAAGACGATATAGTAAATGGGAAAGTTTCGGTGTG 965
Db 1437 CTGCATACTAAGCTTGCCTTTCAAGGATGACTTACTGATTAGCAAGTTTAGTCTCGGT 1496
Qy 966 GATHAAGACCTCTGAACTTATTTGGGATGAGTGGGCAAAATTTTGGAAAGCTTTTC 1025
Db 1497 TCGAAAACGGTGTGCCAGCATGTGTGGGATGAGATTTTCGCTGGCGTTTGGGAAACGCAATTT 1556
Qy 1026 CCACTATCAAGAGAGATGGTGAGCAGGAGAAATCTGGATGTAAGTGAGATGCTCTG 1085
Db 1557 CCCTCCGTGAAGAGAGGCTCTTGAACAGGAACTTATCAGATGGCAGGAGCGCATTA 1616
Qy 1086 AAGATCAAGATCCAGATCTGTATGTACATGGAAGACAGGTTTCGTAGCTGAATACACC 1145
Db 1617 GAGATCAGGCTGCTGATCTATATGTGACCTTCCACACAGATTAAGTACTGAGTACAAG 1676
Qy 1146 AAGTCTGAGGAGTTACCGCATCTAGATATCAAGAGGACTTAGAAGAGCTGAGCAATG 1205
Db 1677 GCCTCTGGACATGCTCGGCTTGACATTAAGGAAGAGATGGAAGAAACCGAAGTGATG 1736
Qy 1206 TACGACCGTTATCAGAAATATCTATCTTAAGGGTCTGATATTTTCGATATCCGGAAG 1265
Db 1737 TACAATGCATTTTCAAGAGTTATCGGTGTTAAGGAGTCTGACAAATTCGATGTTGATGTT 1796
Qy 1266 TTCAAAGACATGTGCAAGGCTTTAGATGTTAGTCCCTGATGTGGCAGACCGAGTAATCGTT 1325
Db 1797 TTTTCCAGATGTGCCAATCTTTGGAAGTTGACCCAAATGACGCGCAGGAGGTTTATAGTC 1856
Qy 1326 GCAGTGGCCGAGATAGAGCGGTTTAACTCTTACTTTTGTATGAAGCCAAACGAGGAGAA 1385
Db 1857 GCGGTCTATGAGCAATGAGAGCGGCTGACTCTCACTTGAACGACCTACTGAGGCGAAT 1916
Qy 1386 GTGGCTAAGGCTCT-----TAAAGACACGCGCTCTGAGGCGGTGATGTTCTTGAACCG 1439
Db 1917 GTTGGCTAGCTTTACAGGATCAAGAGAGGCTTCAGAGGTTGCTTTGGTAGTTTACCTCA 1976

Qy 1440 ACATCCGAGAGGTGAACGCTAAATAAATTTTCTATTGCTGAGAAAGGAGATTCCTGTG 1499
Db 1977 AGAGAAAGTTGAAGAACCGTCCATGAAGGGTTCGATGGCCAGAGAGGAGTTTACAATTAGCT 2036
Qy 1500 TGTGCAGAAAGTCAATGGTTTGACGAATGCTAACTTAGAGCACGAGGAGTTGGAGTCCCTC 1559
Db 2037 GGTCTTGTGTGGAATCATCCGGAGTCGTCTTAATCTTAAGAACGAGGAGATAGAGTCTTTA 2096
Qy 1560 AACGATTTCCATAGGCTTGCCTGGTAGTGTGATTAACAAGCAAAATGGCATCGGTTGTC 1619
Db 2097 GAGCAGTTTCATATGSCAACCGCAGATTCGTTAATTCGTAAGCAGATGAGCTCGATTGTG 2156
Qy 1620 TACATGGCTCTACTCAAGTTCAACAAATGAAGAACTATGTGACAGATTTGGCAGCTTCG 1679
Db 2157 TACACGGGTCGGATTAAGTTTCAGCAAAATGAAAACTTTATCGATAGCTCTGGTAGCATCA 2216
Qy 1680 TTGTCGCCCACTGTATCAAAATCTATGCAAGTCACTAAGGATGAGTCGGGTATGATCT 1739
Db 2217 CTATCTGCTGCGGTGCGAATCTCGTCAAGATCCTCAAGATACAGCTGCTATTGACCTT 2276
Qy 1740 GATTCAGGGGAGAAAGTTGGTGTTCGGGATGTCACTTTGAAAAAGTGGCTCCTCAAACT 1799
Db 2277 GAAACCGCTCAAAAGTTTGGAGTCTTGGATGTTGCATCTAGGAAGTGTGTTAATCAACCA 2336
Qy 1800 GCGGCCAAAGGTCATTCATGGGAGTTGTCCTGGAATTAAGGGGAAAAATGTTTACTGCA 1859
Db 2337 ACGGCCAAGAGTCATGCATGGGCTGTTGTTGAAACCCACGCGAGGAGTATCATGTGGCG 2396
Qy 1860 CTTCTATCTTATGAAGAGATAGAAATGGTGACTGAGAGCAGCTGGAGGAGGTTGGCTGTA 1919
Db 2397 CTTTGGAAATATGATGAGCAGGGTGTGGTGCATGCGATGATTGGAGAGAGTAGTGTGTC 2456
Qy 1920 TCATCTGATACAATGGTATATCTGATATTGCAAGCTCCAAATCTGAGGAAAAACAATG 1979
Db 2457 AGCTCTGAGTCTGTTGTTATTCGACATGCGGAACTCAGAACTCTGCGCAGACTGCTT 2516
Qy 1980 AGAGACGGTGAAACCCACGAACTCTGCAAGAGATGTTACTGTGGATGGGGTCCCTGGT 2039
Db 2517 CGAAAACGAGAACCGCATGTCAGTAGCGCAAGGTTGTTCTTGTGGAAGGAGTTCCGGGC 2576
Qy 2040 TGTGGAAGGTACAAAGGAGATTTTGAAGATTTGATCTTCATGAGGATTTGATCTTCGTT 2099
Db 2577 TGTGGGAAAAACCAAGAAATCTTTCAGGGTTAAATTTTGAAGATCTAAATTTTAGTA 2636
Qy 2100 CTTGGAATAACAAGCTGCTATGATCAGAAAGGAGCTAAATTCATCTGGAAGTGAAGA 2159
Db 2637 CTTGGGAAGCAAGCCGGAATGATCAGAAAGACGTGCGAATTCCTCAGGATTTATTGTG 2696
Qy 2160 GCCAATGGAATAATGTGAGAACGGTAGATTCTCTTAATGCAAT-----CCTAATA 2210
Db 2697 GCCACGAAGGACAACTGTTAAACCGTTGATCTTTCATGATGAATTTTGGGAAAAAGCACA 2756
Qy 2211 CCGGATCACACAAGAGGCTTTTATTTATGAAGAGGTTGATGCTGCACACCGGTTGTT 2270
Db 2757 CGCTGTCAAGTTCAAGAGGTTTATTCATTTGATGAAGGTTGATGTTGCACTCTGTTGTT 2816
Qy 2271 AACTCTCTGTGCTTATCTCTGGTTCGACATCGCATACATTTTACGAGATACACAGCAG 2330
Db 2817 AATTTCTTGTGGCGATGTCATTTGCGAAATTTGCAATATGTTTACGAGAGACACACAG 2876
Qy 2331 ATTCTTTTCAATTAACAGAGTTCAAGATTTCCCGTATCCCAAAACATTTTGAAGAGCTGAA 2390
Db 2877 ATTTCCATACATCAATAGATTTTCAGGATTTCCCGTACCCCGCCCAATTTTGGCAATTTGAA 2936
Qy 2391 GTGATGAAGTTGAGATGAGGAGGACACACACTGAGATGCCAGTGTGATGTAATTTTTC 2450
Db 2937 GTTGAACGAGTGGAGACACAGAACTACTCTCGTTGTCCAGCCGATGTACACATAT 2996
Qy 2451 CTAAATTCGAAGTACGAAGGAGCGGTGAACCACTTTCAATCTGTACAAAGATCCGTTCTCA 2510
Db 2997 CTGAACGAGGAGATAGAGGCTTTGTCTATGAGCACTTCTTCGTTAAAAAAGTCTGTTTCG 3056

QY 2511 TCTGATGATGATGGCGTAAGGAGTACTAAACAGTGTTCCTCAACACCTAAACGGAAA 2570
Db 3057 CAGGAGATGGTGGCGGAGCGCGGTGATCAATCCGATCTCAAAACCCCTTGATGGCAAG 3116
QY 2571 ATTGTAACCTTTCACCTCAGCGCTGATAAATTTGAGTTAGAGGAGACGGCTATAGAGATGTG 2630
Db 3117 ATCTCGACTTTTACCCCAATCGGATAAAGAGCTCTGCTTTCAAGAGGGTATTCAGATGTT 3176
QY 2631 AACACCGTTTCATGAGATCAAGGAGAAACCTTTGAAGATGTCTCGCTGCTCAGATTGACG 2690
Db 3177 CACATCTGTGCATGAAGTGCAGGCGAGACATCTCTGATGTTTCACTAGTTAGGTTAAC 3236
QY 2691 GCAACTCCACTGACTCTGATTTCCAACTCTCCCGCATGTTCTAGTCTGCTCTGACTAGA 2750
Db 3237 CCTACACCACTCTCCATCATTGCAGGAGACAGCCACATGTTTGGTCCGATTGTCAAGG 3296
QY 2751 CACACAAAGAGCTTCAATATTTACACCGTAGTGTGTTAGATCCTTTTAGTACAGTAATAGT 2810
Db 3297 CACACCTGTCTCGCTCAAGTACTACACTGTTGTTATGGATCCTTTTAGTTAGTATCAATTAGA 3356
QY 2811 GATTGTCTCTTTAAGCTCTCTTCTTTTGAAGATGTATATGTAAGATGTAAGCAGGTAGTAGA 2870
Db 3357 GATCTAGAGAACTTAGCTCGTACTTGTAGATATGTAAGGTGATGTCAGGAAACACAA 3416
QY 2871 TAGCAATTAACAGATGGATGAGTGTCAAAGGTCAATCTCTTTGTGCGCAACACCTAAA 2930
Db 3417 TAGCAATTAACAGATGACTCGGTGTTCAAAGGTTCCTCAATCTTTTGTGCGCGCAAG 3476
QY 2931 TCAGAGACTTTCCAGATCTCAGTCTATTAAGATGATGCTCTCGCTGCTGTAATAGTACT 2990
Db 3477 ACTGCTGATATTTCTGATATGAGTGTCTTACTATGATAGTGTCTCCAGGCGCAACGACC 3536
QY 2991 ATACTTAACAGTATGATCTGTACCAAGGTACGTTAGTAAATAGTCTTAAATGTGAAG 3050
Db 3537 ATGATGAATAATTTGATGCTGTACCATGAGGTGACTGACATCTTCATTGATGTCAAA 3596
QY 3051 GATTGTGTTCTTGATTTTCCAAAGTATTCGATGCCAAAGGAGGTGAAACCATGTCTA 3110
Db 3597 GATTGCATATGATATGTTCTAAGTCTGTGTGCGCCTAAGGATCAATCAACCACTA 3656
QY 3111 GAGCAGATTTTGGTACCGCGGGAACCGCCAAAGGCTGCAAGACTACTCGAAATCTG 3170
Db 3657 ATACCTATGTTAGTACGACGCGGAGAAATGCCACGACACTGGACTATTGGAAATTTA 3716
QY 3171 GTTSCAATGATTAAGAAATTTCAACGACACGACCTGACGCGGACGATTCACATTTAG 3230
Db 3717 GTGGCGATGATTAAGAGAACTTTAACGCCACCGAGTTCTGCGCATCAATTGATTTGAA 3776
QY 3231 AGCACCGCATCTGTTGATGATAGTATTTTGTGATGATCTATTTTATTAAGAAAGAAA 3290
Db 3777 AATACCTGATCTTTAGTTGATAGTATTTTGTAGTTATTTGCTTAAGAGAAAGAA 3836
QY 3291 TACACAAAAAATTTCTGAGTGTAGTGAAGAGATCAATGATGAGATGGTTGGAAAC 3350
Db 3837 AAACCAATAAATAATTTCTTTGTTTCACTAGAGAGTCTCTCAATAGATGGTTAGAAAG 3896
QY 3351 AGGAAGAAGTACTATTGACGACTTGGCTTAACATCAATTTTACAGATCTGCGCGCATC 3410
Db 3897 CAGGAACAGGTAACTATGGCCAGCTCGCAGATTTTGTATTTTGGATTTGCCAGAGTT 3956
QY 3411 GATCAGTACAGCAGATGATCAAGGCTCAACCAAAACAGAAATTTGACCTTTCAATTCAG 3470
Db 3957 GATCAGTACAGCAGATGATTAAGCAACAAACCCAGCAAAATTTGACACTTCAATCCA 4016
QY 3471 AATGAATACCTGCTCTGCAAAACAAATTTGCTACCATTCGAAGCAGATCAACGATATTTG 3530
Db 4017 ACGGAGTACCGCGCTTTCAGACGATTTGTGTACCAATTCAAATAAGATCAATGCAATATT 4076
QY 3531 GCGGTTTCT---CAGAGCTTACAGGTTGCTGCTCGAGGCTATTCGATTTCAAGAGTTT 3587
Db 4077 GCGCGCTGTTAGTGAGCTTACTAGGCAATTAACGACAGTGTGTTGATTTGAGCAGATTT 4136
QY 3588 CTTTCTTCTTACTAGGAAACTCCAGAACAGATTTCAAGAATTTTCTCGGATCTCGACTCG 3647

Db 4137 TTGTTTTTCAAGAAAGACACCGAGGATTTAGGATTTCTTCGGAGATCTCCACAGT 4196
QY 3648 CACGTTCTATGATGTGTAGAACTGATATTTCTAAGTATGATAAGTCAAGAACGAG 3707
Db 4197 CATGTCCGATGATGTCTTGGAGCTGATATCAAAATACGACAAATCTCAGATGAA 4256
QY 3708 TTTCAATGTCTGATAGATATGAANAATGGAAGATTTGGGTCTCAATGAGTTTGGCC 3767
Db 4257 TTCCACTGTGAGTAGAATACAGATCTGGCGAAGATTTGGGTTTGAAGACTTCTTTGGA 4316
QY 3768 GAGTGTGGAACAGGCGACAGGAAACAACTTTGAAGGATTAATTCCTGGAATCAAG 3827
Db 4317 GAGTGTGGAACAGGCGCATAGAAAGACCCCTCAAGGATTAACCGCAGGTATAAAA 4376
QY 3828 ACATGCTGTGATCAAGGAAAGCGGTGATGTGACTTCTTTCATCGGCAATACTGTT 3887
Db 4377 ACTTGATCTGTGATCAAGAAAGAGCGGAGCTGACGAGCTTCTTTGGAAACACTGTG 4436
QY 3888 ATAAATAGCAGCTTGTCTGGTCAATGTTACGATGGAAGAGTCAATAAAGGTCCTTTT 3947
Db 4437 ATCATTTGCTGATGTTTGGCCTCGATGCTTCGATGGAAGAAATAATCAAGAGAGCTTT 4496
QY 3948 TGTGAGAGAGTCTCGTTTGTATTTTCCAAAGGTTTGGATTTCCCTGACATTCAGTCA 4007
Db 4497 TCGGTGAGAGTCTGCTGCTGCTTCTTCCAAAGGTTTGTGAGTTTCCGATGTGCAACAC 4556
QY 4008 TGTGTAATCTCATGTGGAATTTTGAAGCCAACTGTATAGAAAGAGTACGCTTACTTT 4067
Db 4557 TCCGGAATCTTATGTGGAATTTTGAAGCAAACTGTTTAAANAACAGTATGATACTTT 4616
QY 4068 TGTGTAGATACATCATCACCATGATAAGGAGCAATAGTGTATATGATCTTTGAAG 4127
Db 4617 TCGGAAAGATATGTAATATACATCAACAGAGAGTCAATGTGTATTAACATCCCTAAAG 4676
QY 4128 TTGATCTCAAACTTTGGGCGAAACATATCAAGGATTAATGATCACTTAGAAGAGTTAAG 4187
Db 4677 TTGATCTCGAACTTTGGTGTCTTAAACATCAAGGATTTGGAAACACTTGGAGAGTTT 4736
QY 4188 GTGCTTTGTGCGATGTTGCTTGTGCTCGGAAACTGCTGCTTAGGCTTTCCGAGCTG 4247
Db 4737 AGGTCTCTTTGTGATGTTGCTGTTTCTGTT---GAACAATTTGCGGTATTACACAGTTG 4793
QY 4248 AACGAGCTATCAAGAGAGTTTCATAAAACCGCATGATGTTGCTGCTTTTAAATGTT 4307
Db 4794 GACGAGCTGATGAGGTTTCATAAGACCGCCTCCAGGTTGCTGTTTCTTTATAAAAGT 4853
QY 4308 GTTAAACAAATTTTGTGTGATTAATTTTATTTAGAACCTTTGTTTAAATGCTGTAG 4367
Db 4854 CTGTTGAAGTATTTGCTGATAAAGTTCTTTTGAAGTTTGTATATAGATGGCTTAGT 4913
QY 4368 TCTCAGAGATCTGTCAAAATTTAGCGAGTTTCATTCATCTTCGAAACAGGATGAGATACT 4427
Db 4914 TGTAAAGGAAAGTGAATATCAATGAGTTTATCGACCTGACAAAATGAGAGATCTT 4973
QY 4428 TCCGCACTTATGACTAAGGTCAAGAGTGTTAGAATAATCGACTGTGGAAGATTAAGC 4487
Db 4974 ACCGTGATGTTTACCCCTGTAAAGAGTGTATGTTTCCAAAGTTGATAAAATAATGCT 5033
QY 4488 TGTAAAGATGATGATCTTTCTGATGATGATTTTACTTAAAGGTTTAACTAGTTAAGAA 4547
Db 5034 TCATGAGAATGAGTCAATTTGTCAGAGGTGAACCTTCTTAAAGAGTTTAACTTATTGATAG 5093
QY 4548 AGGTTATGCTCTTAGCTGATTTTCTGAGTGTCTGGGAGTGGAACTCTCCCGGATAACTG 4607
Db 5094 TGGATACGCTCTGTTTAGCCGTTTGTCTGTCAGGCGAGTGGAACTTCCCTGACAAATTG 5153
QY 4608 CCGTGTGTGTGCTGAGTGTGTTGTTATGATAGAAATGAAGAGGATGAAGAGCAAC 4667
Db 5154 CAGAGAGGTGTGAGGCTGTGCTGTGACAAAGAGTGAAGAGAGCCGACGAGCCAC 5213
QY 4668 GCTGGTGTGATCAACGCGCTGCTTGTGCAAAAGAAATTTTCTTTAAAGCTAATCCCTAA 4727

Db 5214 TCTCGGATCTTACTACACAGAGCTGCAAGAAAGAAATTTCAAGTTCAGTTCGCCA 5273
Qy 4728 TTATTCATTAACATCCGAGGATGCTGAGAACGACCCGTCGCAAGTGTAGTGAATATCAA 4787
Db 5274 TTATGCTATAACCAACCAGGACCGGATGAAAGAGCTCTGCGCAAGTTTGTAGTTAATATTAG 5333
Qy 4788 AGGATGCGCTATGGAAGAAGACTGCTCCTTTATCTTTTGAGAGTTCGTTTCAATTTGTGT 4847
Db 5334 AAATGTGAAGATGTCAGCGGCTTCTCTCGGCTTCTCTGAGTGTGTGTCGCTGTAT 5393
Qy 4848 AGTACATAAAATAATGTAAGAAAGCTTTGAGGGAAGTATTTGAGTGTGACAGACGG 4907
Db 5394 TGTTATAGAAATATATAAATTTAGGTTTGAAGAGAAATATACAAAGTGAAGACGG 5453
Qy 4908 CTCGCCAATTAACCTACTGAAAGGTTGTTTGAGGAGTTCGTTGGAATGAAGTACCAATGGC 4967
Db 5454 AGGCCCATGGAATACAGAGAAGTCTGTTGATGAGTTCATGGAAGATGTCCTCATGTC 5513
Qy 4968 TGTGA 4972
Db 5514 GATCA 5518

RESULT 14

US-10-280-913A-1
; Sequence 1, Application US/10280913A
; Publication No. US20040110130A1

GENERAL INFORMATION:

; APPLICANT: Latgre Scale Biology Corporation
; TITLE OF INVENTION: POPULATION OF POLYNUCLEOTIDE SEQUENCE VARIANTS

; FILE REFERENCE: LSBC-PLGS392-CIP

; CURRENT APPLICATION NUMBER: US/10/280,913A

; CURRENT FILING DATE: 2002-10-25

; PRIORITY APPLICATION NUMBER: 60/402,342

; PRIOR FILING DATE: 2002-08-08

; PRIOR APPLICATION NUMBER: 10/066,390

; PRIOR FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: 60/268,785

; PRIOR FILING DATE: 2001-02-14

; PRIOR APPLICATION NUMBER: 60/266,386

; PRIOR FILING DATE: 2002-02-02

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 10600

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: TMV infectious clone containing CEL I gene

US-10-280-913A-1

Query Match 40.8%; Score 2031; DB 19; Length 10600;

Best Local Similarity 63.6%; Pred. No. 0;

Matches 3169; Conservative 0; Mismatches 1795; Indels 21; Gaps 4;

Qy 6 AAGTAATTCGTAGTTTCAAAGGGAGGCTTTAAAGGTATGACAGAGTTCGCCAAGAA 65
Db 537 AAAACAGTCCCAACTTCCAAAAGGAAGCAATTTGACAGATACGCAAGAAATTCCTGAAGAC 596
Qy 66 GTCTGCTGCTTAAACCTTTTCAGGATTTGCGAATATACCGCCAGAGAAATAGTGTAGA 125
Db 597 GCTGCTGTGTCACATATCTTCCAGCAATGCGGATCAGCGGATGCGAATACGAGCA 656
Qy 126 AGATACGCTGTGCTGCAAGTTTGTATGATATTCCTGTGATGAGTTTGGAGCTGCG 185
Db 657 GTGTATGCCATTGCGCTACAGCATATATGACATACCGCGATGAGTTTCGGGGCGCA 716
Qy 186 TTAATATCTAAGATATACATGATATGATGACGCTTCCATTTTGGCAGAGCATATTATTA 245
Db 717 CTCTTGGAGAAAATGTCCATACGTGCTGTATGCGCTTTTCCACTTCTCTGAGAACTGCTT 776
Qy 246 CTAGACAGAGCGGAGTTACGCTTAATGAATAGCGCAACTTTCAAAAGAGAGAGTGTAT 305

Db 777 CTTGAAGATTTCATACGTCAATTTGGACGAAATCAACGCGTGTGTTTTTCGCGCGATGGAGAC 836
Qy 306 GATGTTTCTTTTTTCTTTGCTGATGAAGTACTTTTAAATATATAGTCATAAATACAAAT 365
Db 837 AAGTTGACCTTTTCTTTTGCATCAGAGAGTACTCTTAAATATATTTGTCATAGTTATCTAAT 896
Qy 366 ATCTTGCAATATGATAGTAAATCTTACTTTCTGCTCTCTAGTAGAATAGTTTACTTTAAG 425
Db 897 ATTCTTAAAGTATGTGTGCAAAACTTACTTCCCGGCTCTAATAGAGAGGTTTACATGAAG 956
Qy 426 GAATTTTTAGTCACTAGGTTTAAATCTTGTTTTGTAATTTTACAAAGTAGATACCTAT 485
Db 957 GAGTTTTTGTACACAGAGTTAATACCTGTTTTGTAAGTTTTCTAGATAGATACCTTTT 1016
Qy 486 ATTCTGTACAAGAGTGTAGACAAGTAGGTTGTGATAGTAGTCAAGTTCATAGAGCGGATG 545
Db 1017 CTTTTGTACAAAGGTGTGCCCCATAAAAGTGTAGATAGTGAGCAGTTTTTATATCTGCAATG 1076
Qy 546 GAAGACGCTTTGCTTTACAAAGAAACCTTTGGCCATGTTCAACACTGAAAGAGCAATCTTT 605
Db 1077 GAAGACGCTATGGCAATTAACAAAAGACTCTTGGCAATGTGCAACAGCGAGAGAATCTCTCTT 1136
Qy 606 AGAGACACGCTTTCGGTTAACTTTTGGTTCCCTAAGATGAAGACATGGGTAGTAGACCG 665
Db 1137 GAGGATTCATCATCACTCAATTAATCTGTTTTCCAAAATGAGGATATGGTCATCGTACCA 1196
Qy 666 CTGTTTTGAGGGTTCTATTACCACAAAAGATGACAAAGGAGTGAGGTCATTTGTTAATCGT 725
Db 1197 TTATTGACATTTCTTTTGGAGACTAGTAAGAGGACGCGCAAGGAAGTCTTAGTGTCCAAG 1256
Qy 726 GACTTCGTTTACAGTGTCTTATCATATCAGAACATATCAAGCCAAAGCGTTAACTTAC 785
Db 1257 GATTTCTGTTTACAGTGTCTTAAACCATTCGAAACATACACAGCGAAAGCTCTTACATAC 1316
Qy 786 CAGAACGTATTATCTTTCTGGAGTCTATAAGATCCCGCTGATATCAATGTTGTTACT 845
Db 1317 GCAATGTTTTGTCCTTTGTCGAATCGATTCGATCGAGGTTATCATTAAACGGTGTGACA 1376
Qy 846 GCTAGGTCGAATGGGATGATGATAAGCAATTTCTTCAACCTTGTCAATGACTTTCTTC 905
Db 1377 GCGAGGTCGAATGGGATGAGCAAAATCTTTGTACAAATCTTTGTCATGACGCTTTTAC 1436
Qy 906 TTGACACTAAGCTGCGCTTCAAGACATATAGTAAATGGAAGTTTTCGGTGTCTG 965
Db 1437 CTGCATCTAAGCTTCCGCTTCAAGAGGATGACTTACTGATAGCAAGTTTAGTCTCGGT 1496
Qy 966 GATAAGACCACTTCTGAACCTTATTTGGGATGAGTGGGCAAAATTTTTTGGAAACGTTTTTC 1025
Db 1497 TCGAAAACGGTGTGCCAGCATGTGTGGATGAGATTTCCGCTGGGCTTTGGAAACGCAATT 1556
Qy 1026 CCACATATCAAAGAGAGATTTGGTGAGCAGGAAAATTTCTGGATGTAGTGAATGCTCTG 1085
Db 1557 CCCTCCGTGAAAAGAGAGGCTCTTGAACAGGAAACTTATCAGAGTGGCAGCGACGCAATTA 1616
Qy 1086 AAGATCAAGATCCAGATCTGTATGTCACATGAAAGACAGGTTTCGTAGCTGAATACACC 1145
Db 1617 GAGATCAGGGTGCCTGATCTATATATGACCTTCCACACAGATTTAGTACTGAGTACAG 1676
Qy 1146 AAGTCTGAGGAGTTACCGCATCTAGATATCAAGAAGACTTAGAAGAGCTTAGAAGCAATG 1205
Db 1677 GCCTCTGTGACATGCTCGCTTGACATTTAGGAAGAAGATGGAAGAAACGGAAGTGTATG 1736
Qy 1206 TAGACGCGTTATCAGAAATTTATCTATCTTAAAGGGTCTGATTAATTTTCGATATCCGGAAG 1265
Db 1737 TACAATGCACTTTTCAAGTTTATCGGTGTTAAGGGAGTCTGACAAATTTCTGATTTGATGTT 1796
Qy 1266 TTCAAAGACATGTGCAAGGCTTTAGATGTTAGTCTCTGATGTGGCAGCACGAGTAATCGTT 1325
Db 1797 TTTTCCAGATGTGCCATCTTTGGAAGTTGACCCATGACGCGAGCGAAGGTTATAGTC 1856
Qy 1326 GCAGTGGCCGAGAAATAGAAGCGGTTTAACTCTTTATCTTTTGAATAGCCAAACGAGAGAAAT 1385
Db 1857 GCGGTCTATGACCAATGAGAGCGGTCTGACTCTCACATTTGAAACGACCTACTCTGAGCGCAAT 1916


```
Db 4077 GGGCCGTTGTTAGTAGCTTACTAGGCAATTAATCTGACAGTGTGTGATTCGAGCAGATTT 4136
Qy 3588 CTTTCTTTTACTAGGAAACTCAGAACAGATTCAAGAAATTTTCTCGGATCTCGACTCG 3647
Db 4137 TTGTTTTTCAAGAAAGACACAGCGCAGATTGAGGATTTCTTCGGAGATCTCGACAGT 4196
Qy 3648 CACGTTCTCTATGATGTTGTAGAACTGGATATTTCTAAAGTATGATAAGTACAGAACGAG 3707
Db 4197 CATGTGCGGATGATGTTCTTGGAGCTGGATATATCAAAATACGACAAATCTCAGAAAGAA 4256
Qy 3708 TTTCAATGCTCTAGAGTATGAATATGAAAGATTTGGGTCTCAATGATTTTGGCC 3767
Db 4257 TTTCACTGTGAGTATGAGATCTGCGAAGATTGGGTTTTTGAAGACTTCTTGGGA 4316
Qy 3768 GAAGTGTGAAACAAAGGCGACAGGAAACAACTTTGAAGGATTACATTTGCTGGAATCAAG 3827
Db 4317 GAAGTTTGGAAACNAGGGCATAGAAAGCACCCCTCAAGGATTTATACCGCAGGTATAAAA 4376
Qy 3828 ACATGCTGTGTTATCAAGGAAAGCGGTGATGTGACTACTTTCAATCGGCAATACGTTT 3887
Db 4377 ACTTGCACTCTGGTATCAAGAAAGAGCGGAGCGTACGACGTTCTATTGGAACACCTGTG 4436
Qy 3888 ATATAGCAGCTTCTTGGGTTCAATGTTACCGATGGAAGGTCATAAAGGTGCTTTT 3947
Db 4437 ATCATGCTCGATGTTTGGGCTCGATGCTTCCGATGGAGAAATTAATCAAGAGGCGCTTT 4496
Qy 3948 TGTGGAGACGATTCGCTTTTGTATTTTCCAAAGGGTTTGATTTCCCTCGACATTCAGTCA 4007
Db 4497 TCGGTGACGATAGTCTGTGACTTTTCCAAAGGGTTGTGAGTTTCCGGATGTGCAACAC 4556
Qy 4008 TGTGCTAATCTCATGTGGAAATTTTGGGCCCAAACTGTATAGAAAGAGTACGGTTACTTT 4067
Db 4557 TCCGCGAATCTATGTGGAATTTTGAAGCAAACTGTTTAAAAAACAATATGGATACTTT 4616
Qy 4068 TGTGGTAGATACATACATACACATGATAGGGAGCAATAGTGTATATGATCCTTTGAAG 4127
Db 4617 TCGGGAAGATATGTAATACATACGACAGAGGATGCAATTTGTATATACGATCCCTAAAG 4676
Qy 4128 TTGATCTCCAAACTTGGGGCAAAACATATCAAGGATTATCATCTTTAGAAAGATTAAAG 4187
Db 4677 TTGATCTCGAACTTGGTGCTAAACATACAGATTTGGGAACATTTGGAGGATTCAGA 4736
Qy 4188 GTGTCTTTGTGCGATGTTGCTGTGCTCGGAACTGGTGCTTAGGCTTTCCGCAAGCTG 4247
Db 4737 AGGTCTCTTTGTGATGTTGCTGTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTT 4793
Qy 4248 AACCGACTATCAAGGAGGTTTCATAAACCGCGATTGATGGTTCGTTTCTTTTAAATGT 4307
Db 4794 GACGACGCTGTATGGGAGGTTTCATAAGACCGCCCTCCAGGTTGCTTTGTTTATAAAAGT 4853
Qy 4308 GTTAAACAAATTTTGTGCTGATAAATTTTATTAAGAACTTTGTTTAAATGGCTGTAG 4367
Db 4854 CTGTTGAAGTATTTGCTGATAAAGTTCTTTTGAAGATTTGTTTATAGTGGCTTAGT 4913
Qy 4368 TCTCAGAGATCTGCTCAAAATTTAGCGAGTTCATTTGATCTTTTCGAAACAGGATGAGTACT 4427
Db 4914 TGTTAAAGGAAAGTGAATATCAATAGATTTATCGACCTGACAAAAAATGGAGAAGACTTT 4973
Qy 4428 TCCGGCATTATGATCAAGTCAAGTGTAGAAATATCGACTGTGCAAGATTTATGGC 4487
Db 4974 ACCGTCGATGTTTACCCCTGTAAAGAGTGTATGTTGTTCCAAAGTTGATATAAATAATGGT 5033
Qy 4488 TGTTAAGAAATGATAGTCTTTCTGATGTAGATTTTAAAGGTTCTTAAGTTTAGTTAAGAA 4547
Db 5034 TCATGAGAAATGAGTCATTTGACAGAGGTGAACCTTTCTTAAGGAGTTAAGCTTTATGTAG 5093
Qy 4548 AGGATATGTGTGCTAGTATTTGGTAGTGTCTGGGAGTGGAAATCTCCCGGATAACTG 4607
Db 5094 TGGATACGTCGTTTGTAGCCGTTTGGTTCGTACCGGCGAGTGGAACTTGCCTGCAAAATG 5153
Qy 4608 CCGTGGTGGTCACTGTTTGTATTTGATAGTAAGAAATGAAGAGGAGTAGAAGGACAC 4667
```

```
Db 5154 CAGAGAGAGTGTGAGCGTGTGTCTGTGTGGACAAAAGATGGAAGAGCCGACGAGGCCAC 5213
Qy 4668 GCTGGGTGGCTATCACGCCCTCTCTTTGCAAAAAAGAAATTTTCTTTTAAGCTAATCCCTAA 4727
Db 5214 TCTCGGATCTTACTACACAGCAGCTGCAAAAGAAAGATTTTCAAGTTCAGGTCTGTCCTCA 5273
Qy 4728 TTATTCATTAACATCCGAGGATGCTGAGAAGACCCGTCGSCAAGTGTGTAGTGAATATCAA 4787
Db 5274 TTATGCTATAAACCAACCCAGGACGCGATGAAAAACGCTCGCAAGTTTTTGTAGTTAATATAG 5333
Qy 4788 AGGAGTGGCTATTCGAAAGAGGATCTGCTCTTTATCTTTTGGAGTTCGTTTCAATTTCTGT 4847
Db 5334 AAATGGAAGATGTCAGCGGTTTCTGTCGCTTTCTCTGGAGTTTGTGTGCGTGTAT 5393
Qy 4848 AGTACATAAAAAATAATGTAAGAAAAAGTTTGGAGGAACGTTATTTTGGAGTGTGACAGACGG 4907
Db 5394 TGTTTATAGAAATAATATAAAATTTAGGTTTGGAGAGAGAGATTTACAAACGTCGAGAGACGG 5453
Qy 4908 CTCGCCAATTTGAATCACTCACTGAAAAAGGTTGTGTAGGAGTTTGTGATGATGACCAATGGC 4967
Db 5454 AGGGCCCATGGAACCTTACAGAAAGAGTTCGTTGATGAGTTTCATGGAAGATGTCCCTATGTC 5513
Qy 4968 TGTGA 4972
Db 5514 GATCA 5518
```

RESULT 15

```
US-10-684-134-1
; Sequence 1, Application US/10684134
; Publication No. US20040142433A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: POPULATION OF POLYNUCLEOTIDE SEQUENCE VARIANTS
; FILE REFERENCE: LSBC-PLG5392-CIP
; CURRENT APPLICATION NUMBER: US/10/684,134
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/402,342
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 10/066,390
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/268,785
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/266,386
; PRIOR FILING DATE: 2002-02-02
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMV infectious clone containing CEL I gene
US-10-684-134-1
```

```
Query Match 40.8%; Score 2031; DB 19; Length 10600;
Best Local Similarity 63.6%; Pred. No. 0;
Matches 3169; Conservative 0; Mismatches 1795; Indels 21; Gaps 4;

Qy 6 AAGTAAATTCCTGAGTTTCAAGGGAGGCTTTTAAACAGGTATGCAAGAGCTCCCAACGAA 65
Db 537 AAAACAGTCCCAACTTCCAAAAGGAAGCAATTTGACAGATACGCAAGAAATTCCTGAAGAC 596
Qy 66 GTCTGCTGCTCTAAAACTTTTTCAGGATTTGTGCAATACATCCGCCAGAGAAATAGTGGTAGA 125
Db 597 GCTGTCTGTCACAATCTTTCCAGACAATCGCATCAGCCGATGCGCAATCAGGACAGA 656
Qy 126 AGATACGCTGTTGCTGTGCAAGTTTGTATGATATTCCTGTGCAATGATGATTTGGAGCTGCG 185
Db 657 GTGTATGCCATTCGCTGTACACAGCATATATGACATACCAGCCGATGATGTTGGGGCGGCA 716
Qy 186 TTAATATCTAAGAAATATACATGATGTTATGTCAGCTTCCATTTTGGCAGAGCAATATTATA 245
```


Db 717 CTCCTTGAGAAAAATGTCCATACGTGTCTATGCGCTTTCCACTTCTCTGAGAACCTGCTT 776
Qy 246 CTAGACCAAGCGGAGTTACGTTTAATGAATAGCGGCACTTTCAAAGAGAGGTGAT 305
Db 777 CTTGAAGATTTCATACGTCAAATTTGACGAAATCAACGCGTGTGTTTTCGCGGATGGAGAC 836
Qy 306 GATGTTCTTTTCTTTCTGCTGATCAAAAGTACTTTAAATATTAGTACATAAAATACAAAAAT 365
Db 837 AAGTTGACCTTTCTTTTGGCATCAGAGAGTACTCTTAATATTGTCTAGTATTCTTAAT 896
Qy 366 ATCTTGCAATATGTAGTTAAATCTTACCTTCTGCTCTCTAGTAGAATAGTTTACTTTAAG 425
Db 897 ATTCTTAAGTATGTGCAAAACTTACTTTCCGCGCTCTTAATAGAGAGGTTTACATGAAG 956
Qy 426 GAAATTTTGTAGTCACTAGGTTAACTTTGTTGTTTGTAAATTTTACCAAGTAGATACCTAT 485
Db 957 GAGTTTGTAGTCACAGAGTTTAATACCTGTTTGTAAATTTTCTAGAAATAGTACTTTT 1016
Qy 486 ATTCTGTACAAGAGTTTACACAAGTAGGTTGTAGTAGTCACTGTTCTATGAGCGATG 545
Db 1017 CTTTGTGTAAGAAGTTGTGCCCATAAAGTGTAGATAGTACGAGTTTATATCTCAATG 1076
Qy 546 GAAGACGCTTTGCTTACAGAAAACTTTGGCCATGTTCAAACACTGAAGAGCAATCTTT 605
Db 1077 GAAGACGCTTGCATTTACAAAAAGACTTTGCAATGTGCAACAGCGAGAGAAATCTCTT 1136
Qy 606 AGAGACAGGCTTGGTTAACTTTTGGTTCCCTAGATGAAGGACATGTTGATAGTACCG 665
Db 1137 GAGGATTCATCATCATGCTAACTTACTGTTTCCCAAAATGAGGATATGTCATCGTACCA 1196
Qy 666 CTGTTGTAGGTTCTATACAGCAAAAGATGACAAGAGTGAGGTCAATGTTAATCGT 725
Db 1197 TTATTCGACATTTCTTTGAGACTAGTAAGAGGACCGCGAAGAGTCTTAGTGTCCAG 1256
Qy 726 GACTTCGTTTACACAGTGTCTTAATCATATCAGAACATATCAAGCCAAAGCGTTAACTTAC 785
Db 1257 GATTTGCTGTTTACAGTGTCTTAACCACTTCAACATACACGCGAAGCTCTTACATAC 1316
Qy 786 CAGAACGTTATATCTTTGCGGAGTCTATAAGATCCGCGTGTATCAATCAATGGTGTACT 845
Db 1317 GCAAAATGTTTGTCTTTGTCGAATCGATTCGATCGAGGTAATCAATTAACGCGTGTACA 1376
Qy 846 GCTAGTCTGAATGGGATGTAGATAAGCAATTTCTTCAACCTTGTCAATGACTTTCTTTC 905
Db 1377 GCGAGTCCGAATGGGATGTGACAAATCTTTGTTACATCTTTGTCATAGAGTTTAC 1436
Qy 906 TTGCACTAAGCTGCGCTTCAAGACGATATAGTAATGGAAGGTTTTCGTCGCTTG 965
Db 1437 CTGCACTAAGCTTCCGCTTCTTAAAGGATGACTTACTGATTAGCAAGTTTAGTCTCGT 1496
Qy 966 GATAAGACCACTTCTGAACTTATTTGGGATGAGTGGGCAATTTTTCGNAACGTTTTC 1025
Db 1497 TCGAAACCGTGTGCCAGCATGTGTGGGATGAGATTTCGTCGCGTTTGGGAACGCAATT 1556
Qy 1026 CCCACTATCAAGAGAGATTGGTACGAGAAATTTCTGATCTAAGTAGAGATGCTCTG 1085
Db 1557 CCTCCGTGAAGAGAGGCTCTTGAACAGAACTTATCAGATGGCAGCGCAGCATTA 1616
Qy 1086 AAGATCAAGATCCAGATCTGTATGTACATGGAAGACAGAGTTTCGTAGCTGAATACACC 1145
Db 1617 GAGATCAGGTTGCTGATCTATATGTGACCTTCCACGACAGATTAGTACTGAGTACAAG 1676
Qy 1146 AAGTCTGAGAGTTACCGCATCTAGATATCAAGAGGACTTGAAGAGCTGAGCAATG 1205
Db 1677 GCCTCTGTGACATGCTGCGCTTGACATTTAGGAAGAAGATGAAGAAACGGAAGTGTG 1736
Qy 1206 TAGACCGGTTATCAGAAATTTATCTTCCCTTAAGGTTCTGATATTTTCGATATCGCGAAG 1265
Db 1737 TACAATGCACTTTTACAGATTATCGGTGTTAAGGAGTCTGACAAATTCGATGTTGATGTT 1796
Qy 1266 TTCAAGACATGTGCAAGGCTTTAGATGTTTGTAGTCTGATGTGGCAGCACAGTAATCGTT 1325
Db 1797 TTTTCCAGATGTGCCAATCTTTGGAAGTTGACCCCAATGACCGGAGGTTATAGTC 1856

Qy 1326 GCAGTGGCCGAGAAATAGAAAGCGGTTTAACTCTTACTTTTGTAAACCAACCGAGAGAAAT 1385
Db 1857 GCGGTATGATGCAATGAGAGCGGCTGACTCTCTCAATTTGAACCGACTTACTGAGCGAAT 1916
Qy 1386 GTGGCTAAGGCTCT-----TAAAGACAGCGGCTGAGCGGCTGATGCTTCTTGAACCG 1439
Db 1917 GTTGGCTTAGCTTTACAGGATCAAGAGAAGCTTTCAGAAAGGTGCTTTGGTAGTTACCTCA 1976
Qy 1440 ACATCCGAAGAGGTGAACGTAAATTAATTTTCTATTGCTGAGAAAGGAGATTTGCTGTG 1499
Db 1977 AGAGAGTTGAAGAACCGTCCATGAGGGTTTCGATGGCCAGAGGAGATTACAAATAGCT 2036
Qy 1500 TGTGAGAAAGTCAATGTTTGAAGAACTCTAACTTTAGAGCACCGAGAGTTGAGCTCCCTC 1559
Db 2037 GGTCTGCTGAGATCATCCGAGTCTGCTTATTCTAAGAACGAGAGATAGAGTCTTTA 2096
Qy 1560 AACGATTTCCATAGGCTTGGTGGATGTGATTACAAAGCAATGCGATCGGTTGTC 1619
Db 2097 GAGCAGTTTTCATATGCAACCGCAGATTCGTTAAATTCGTAAGCAGATGAGCTCGATTG 2156
Qy 1620 TACACTGCTCACTCAAAAGTTCAACAAATGAAGAACTATGTGCAAGAGTTTGGCAGCTTCG 1679
Db 2157 TACACGGTCCGATTAAGTTTCAAGAACTTTATCGATAGCTGCTGATGATCA 2216
Qy 1680 TTGTCGCGCACTGTATCAAACTTATGCAAGTCACTAAAGGATGAAGTGGGTATGATCT 1739
Db 2217 CTATCTGCTGGTGTGCAATCTCGTCAAGATCTTCAAGATACAGCTGCTATTGACCTT 2276
Qy 1740 GATTCAGGAGAAAGTTGGTGGATGTACCTTTGAAAGAGTGGCTCTCAAACT 1799
Db 2277 GAAACCCGTCAAAAGTTTGGAGTCTTGGATGTGATCTAGGAAGTGGTTAATCAAAACCA 2336
Qy 1800 GCGGCCAAAGTCAATTCATGGGAGTGTCTGGATTACAAGCGGAAATGTTTACTGCA 1859
Db 2337 ACGGCCAAAGTCAATTCATGGGAGTGTGTGAAACCCACCGAGGAAATGATCATGTGGG 2396
Qy 1860 CTTCTATCTTAAAGAGAGATAGAAATGGTGAAGTCTGAGAGCGACTGAGGAGGTTGGCTGTA 1919
Db 2397 CTTTGGAAATATGATGAGCAGGCTGTGTGATGATCGATGATGGAGAGAGTAGCTGTC 2456
Qy 1920 TCATCTGATCAATGGTATATCTGATATGCAAGCTTCAAAATCTGAGGAGGTTGGCTGTA 1979
Db 2457 AGCTCTGAGTCTGTTTATTTCCGACATGGCGAACTCAGAACTCTGCGACAGCTGCTT 2516
Qy 1980 AGAGCGGTGAACCCACGAACTTACTGCAAGAGTGTACTTGTGATCGGCTGCTGCTGCT 2039
Db 2517 CGAAACGGAGAACCGCATGTCAAGTCCGCAAGAGTGTCTTGTGACGAGTTCGCGG 2576
Qy 2040 TGTGAAAGTACAAGAGGAGATTGAAAGATTGATCTTGTGATGAGGATTGATCTTGGTT 2099
Db 2577 TGTGGGAAACCAAGAAATCTTCCAGGTTAATTTTGTATGAAGATCTAATTTTGTAGTA 2636
Qy 2100 CTTGAAACCAAGTCTGCTATGATCAGAAAGGCTTAAATTCATCTGAGCTGATGAAGA 2159
Db 2637 CTTGGAAGCAAGCCGCAAAATGATCAGAAAGTGGCAATTCCTCAGGAGTATTGTTG 2696
Qy 2160 GCCAATCGCAATGTGAGAACGCTGATGATCTTCTAATGCT-----CAAAA 2210
Db 2697 GCCAAGAGGACAAAGTTTAAACCGTTGATCTTTTCATGATGAATTTTGGGAAAGCACA 2756
Qy 2211 CCGCATCACAAGAGGCTTTTATTTGATGAAGGTTGATGCTGACACCGGTTGTT 2270
Db 2757 CGCTGTGATCAAGAGGTTTATTCATTTGATGAAGGTTGATGTTGATCTGCTGTTGTT 2816
Qy 2271 AACTTCCTGCTTATCTCTGTTGCGCATCGCATACATTTACGAGATACACAGCAG 2330
Db 2817 AATTTTCTTGTGCGATGTCAITGTGCAAAATGTCATATGTTTACGAGACACACAGCAG 2876
Qy 2331 ATTCTTTTCATTAACAGAGTTCAGAAATTTCCGCTATCCCAACATTTTGAAGAGCTGCAA 2390
Db 2877 ATTCCATACATCAATAGAGTTTCAGATTCCCGTACCCCGCCCATTTTTCGCAAAATGGA 2936


```

Db 5094 TGGATACGTCCTGTTTGGTCGTCACGGCGGAGTGGAACTTGCCTGACAAATTG 5153
Qy 4608 CCGTGGTGGTGTCACTGTTTGTATTGTAGATAAGAGATGAAAAGAGTAAAGGAAGCAAC 4667
Db 5154 CAGAGGAGGTGTGACGGTGTCTCGTGGACAAAGAGATGGAAGAGCCGACGAGGCCAC 5213
Qy 4668 GCTGGGTGCGTATCACGCGCCCTGCTTGCACAAAGAAATTTTCTTTAAAGCTAAATCCCTAA 4727
Db 5214 TCTCGATCTTACTACACAGCAGCTGCAAGAGAAAGATTTCAAGTTCGAAGTCTGCCAA 5273
Qy 4728 TTATTCAATAACATCCGAGGATGCTGAGAGACCCGTTGGCAAGTGTAGTGAATATCAA 4787
Db 5274 TTATGCTATAACACCCAGGACCGATGAAAAACGCTCGGCAAGTTTGTAGTTAATATTAG 5333
Qy 4788 AGGAGTGGCTATGGAAGAAGGATACGTCTCTTTATCTTTGGAGTTCGTTTCAATTTGT 4847
Db 5334 AAATGTGAAGATGTGAGCGGTTTCTGTCGGCTTTCTCTGGAGTTTGTCTGGTGTAT 5393
Qy 4848 AGTACATAAAATAATGTAAGAAAAAGTTTGAAGGAACGTATTTTGAAGTGTGACAGCG 4907
Db 5394 TGTATTAGATAATATAAATTTAGTTTGAAGAGAAAGATTACAAACGTGAGAGACGG 5453
Qy 4908 CTCGCCAATTGAATCACTGAAAGAGTTGTTGAGGAGTTCGTGGATGAAGTACCAATGGC 4967
Db 5454 AGGGCCCATGGAACCTTACAGAAAGATCGTTGATGAGTTTCATGGAAGATGCCCTATGTC 5513
Qy 4968 TGTGA 4972
Db 5514 GATCA 5518

```

Search completed: July 28, 2005, 18:44:52
 Job time : 1905.98 secs

